

# SEQUENCE LISTING

<110> Messier, Walter

<120> Methods to Identify Evolutionarily Significant Changes in Polynucleotide and Polypeptide Sequences in Domesticated Plants

<130> GENO200.1/CIP

<150> US 09/240,915

<151> 1999-01-29

<150> US 60/349,088

<151> 2002-01-16

<150> US 09/368,810

<151> 1999-08-03

<150> US 09/875,666

<151> 2001-06-06

<150> US 60/315,595

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<170> PatentIn version 3.1

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caaccacaca acaccgaaat gatggtgaga acagcatcaa cccagcagca aagcatcaaa	1680
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gtcgatgttc ctccatctat gagggcatca aaggaaaggg ttggccttcg tcctgcagag	1800



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gctaaggTTA cacaagagT tgatcctCCA cctGCCaagg catctcagag aattgatcct 1920
ctgttgccat ccaaggTTca tatagatgct actcgatctt ttacgaaggT ctcccagaca 1980
gagatcaagc cggaagtaca gcccCaatt ccgaaggTgc ctgtggctat gcctaccatc 2040
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg
35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His
50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg
65 70 75 80

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aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser 100 105 110	336
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro 115 120 125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg 130 135 140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val 145 150 155 160	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys 165 170 175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
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aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
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Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
305 310 315 320

aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc 1008  
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
325 330 335

tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc 1056  
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
340 345 350

aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag 1104  
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
355 360 365

ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat 1152  
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
370 375 380

gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa 1200  
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
385 390 395 400

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act 1248  
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
405 410 415

tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta 1296  
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
420 425 430

cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1341  
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<211> 446

<212> PRT

<213> Oryza sativa cv. Teqing

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Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg  
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
50 55 60

206T20" 2405200T

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
275 280 285

206T20 24054001

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro  
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
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Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
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<213> Oryza sativa cv. Lemont

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gtgtgatccg ggggtgaggt taggcgggac gccggggcat cagccatgtc gaggtgcttc 180  
ccctaccgcg cgccggggta cgtgcgaaac ccagtgggtg ccgtggccgc ggccgaagcg 240  
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gctcttgccct gttgggttttg atcggatctg ttgggtgtgo gtgtgtgatt tggggatcgc 360  
acgtgcggggg aagctaacct ttgcatggat aacttgagat ttgtgaggcc gcgcttcgac 420  
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<213> Oryza sativa cv. Lemont

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atcagaactg acgattgctc tgggtggctga agctccagaa agaaagggaa aaggctgaaa 240  
agaagaaaga gaaaaggagt gacaggaaag ctcttccaca tggtagata tccaagcatt 300  
caaagcgaac ccaccacaag aagagaaaac atgaagacat caataatgct gatcagaagt 360  
cccgaagggt ttcttccatg gaacctgggtg agcaattgga gaagagtgga ctctcagaag 420  
agcatggagc tccttgcttt actcagacag agcatggctc tccagagagt tcacaggaca 480  
gcagcaagag aagaaagggt gtgttaccca gtcctagcca agctaagaat ggtgaggccc 540  
tttcttgcat ttgtcttctt ttagctgggtg atgttgaatt ggtttgactt atcctgaatt 600  
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ccctttcgga gaaatctaatt gttgtacaaa caccagttca tcaaatggga tcagtttcat 720  
ctctgccaaag taagaaaaac tcaatgcaac cacacaacac cgaaatgatg gtgagaacag 780  
catcaaccca gcagcaaagc atcaaagggtg attttcaagc agtaccgaaa caaggatatgc 840  
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 gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96  
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30  
 aaa gaa agg gaa aag gct gaa aag aag aaa gag aaa agg agt gac agg 144  
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
 35 40 45  
 aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192  
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
 50 55 60  
 cac aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc 240  
 His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser  
 65 70 75 80  
 cgg aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga 288  
 Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly  
 85 90 95  
 ctc tca gaa gag cat gga gct cct tgc ttt act cag aca gag cat ggc 336  
 Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly  
 100 105 110  
 tct cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta 384  
 Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu  
 115 120 125  
 ccc agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata 432  
 Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile

130	135	140	
aga aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt			480
Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val			
145	150	155	160
gta caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt			528
Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser			
	165	170	175
aag aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca			576
Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr			
	180	185	190
gca tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ccg			624
Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro			
	195	200	205
aaa caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt			672
Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val			
	210	215	220
cct cca tct atg agg gca tca aag gaa agg att ggc ctt cgt cct gca			720
Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala			
	225	230	240
gag atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att			768
Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile			
	245	250	255
gtc aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct			816
Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro			
	260	265	270
gcc aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat			864
Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His			
	275	280	285
ata gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag			912
Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys			
	290	295	300
ccg gaa gta cag ccc cca att ctg aag gtg cct gtg gct atg cct acc			960
Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr			
	305	310	315
atc aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc			1008
Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys			
	325	330	335
tcc tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag			1056
Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln			
	340	345	350
tcc aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag			1104
Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys			
	355	360	365



aag ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg 1152  
Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met  
370 375 380

gat gat atg gat ctc ggg gac cag gat tgg ctg ctt gat agt acg agg 1200  
Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg  
385 390 395 400

aaa cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt 1248  
Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu  
405 410 415

act tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat 1296  
Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His  
420 425 430

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<211> 447

<212> PRT

<213> Oryza sativa cv. Lemont

<400> 13

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
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20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
50 55 60

His Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser  
65 70 75 80

Arg Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly  
85 90 95

Leu Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Glu His Gly  
100 105 110

206720-2406200T

Ser Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu  
115 120 125

Pro Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile  
130 135 140

Arg Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val  
145 150 155 160

Val Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser  
165 170 175

Lys Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr  
180 185 190

Ala Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Pro  
195 200 205

Lys Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val  
210 215 220

Pro Pro Ser Met Arg Ala Ser Lys Glu Arg Ile Gly Leu Arg Pro Ala  
225 230 235 240

Glu Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile  
245 250 255

Val Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro  
260 265 270

Ala Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His  
275 280 285

Ile Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys  
290 295 300

Pro Glu Val Gln Pro Pro Ile Leu Lys Val Pro Val Ala Met Pro Thr  
305 310 315 320

Ile Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys  
325 330 335

Ser Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln

340

345

350

Ser Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys  
 355 360 365

Lys Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met  
 370 375 380

Asp Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Asp Ser Thr Arg  
 385 390 395 400

Lys Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu  
 405 410 415

Thr Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His  
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Leu Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
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<211> 2459

<212> DNA

<213> Oryza sativa strain IR64

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cgtgccggat catttgctct tgccgtgttg ttttgatcgg atctgttggt tgtgcgtgtg	180
tgatttgggg atcgcacgtg cggggaagct aacctttgca tggataactt gagatttgtg	240
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tctcggttatt ggtgtgttac gagtaacctg tgtgttgtaa tctccgcttg gactagattc	600
caagtaatcc agtgccttca tgacctgcaa attctatgcc tatgaagtaa catgaacagt	660
ttgtatgtat tctgttgatg catacttgca ttatttgtga gatgtacatg ttgtggtaaa	720

atattgcatt caccatatag aaatagtaat tgactatcct tgttttagttc gaaaactact	780
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tgtgactaac catgtaacaa atatattaag gattatcaaa ttattctatg tgaagtgtcc	900
gtgccctaata tgtgttatct tctgtaactg atagcacaac atttgtttcc tgctgtgtgc	960
ttgtgtaaat tgggtacttca tcattactat atatttcaaa gaaaattctg cattgcattc	1020
ccgtcgtccg ttctaaatca gaactgacga ttgctctggt ggctgaagct ccagaaagaa	1080
agggaaaagg ccgaaaagaa gaaagagaaa aggagtgcga ggaaagctct tccacatggt	1140
gagatatcca agcattcaaa gcgaacccac aagaagagaa aacatgaaga catcaataat	1200
gctgatcaga agtcccggaa ggtttcctcc atggaacctg gtgagcaatt ggagaagagt	1260
ggactctcag aagagcatgg agctccttgc ttactcaga cagtgcattg ctctccagag	1320
agttcacagg acagcagcaa gagaagaaag gttgtgttac ccagtcctag ccaagctaag	1380
aatggtgagg ccctttcttg catttgtctt ctttttagctg gtgatgttga attgggttga	1440
cttatcctga attatcatct tgcaggtaac atccttcgaa taaagataag aagagatcaa	1500
gattcttcag cttccctttc ggagaaatct aatggtgtac aaacaccagt tcatcaaag	1560
ggatcagttt catctctgcc aagtaagaaa aactcaatgc aaccacacaa caccgaaatg	1620
atggtgagaa cagcatcaac ccagcagcaa agcatcaaag gtgattttca agcagtactg	1680
aaacaaggta tgccaacccc agcaaaagtc atgccaagag tcgatgttcc tccatctatg	1740
agggcaccaa aggaaagggg tggccttcgt cctgcagaga tgttggccaa tgttggtcct	1800
tcaccctcca aggcaaaaca gattgtcaat cctgcagctg ctaagggttac acaaagagtt	1860
gatcctccac ctgccaaggc atctcagaga attgatcctc tgttgccatc caagggtcat	1920
atagatgcta ctgatcttt tacgaagctc tcccagacag agatcaagcc ggaagtacag	1980
ccccaattc cgaagggtgc tgtggctatg cctaccatca atcgtcagca gattgacacc	2040
tcgcagccca aagaagagcc ttgctcctct ggcaggaatg ctgaagctgc ttcagtatca	2100
gtagagaagc agtccaagtc agatcgcaaa aagagccgca aggctgagaa gaaagagaag	2160
aagttcaaag atttatttgt tacctgggat cctccgtcta tggaaatgga tgatatggat	2220
cttggggacc aggattggct gcttggtagt acgaggaaac ctgatgctgg cattggcaac	2280
tgcagagaaa ttgttgatcc acttacttct caatcagcgg agcagttctc attgcagcct	2340
agggcgattc atttaccaga cttcatgtc tatcagttgc catatgtggt tccattctag	2400
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<210> 15  
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 <213> Oryza sativa strain IR64

<220>  
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 atg tcg agg tgc ttc ccc tac ccg ccg ccg ggg tac gtg cga aac cca 48  
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96  
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144  
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192  
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
 50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cg 240  
 Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
 65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288  
 Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
 85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336  
 Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
 100 105 110

cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc 384  
 Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
 115 120 125

agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga 432  
 Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Arg Ile Lys Ile Arg  
 130 135 140

aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta 480  
 Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
 145 150 155 160

caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag 528  
 Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
 165 170 175

aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200

cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act 1248  
 Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
                   405                  410                  415

tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta 1296  
 Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
                   420                  425                  430

cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag 1341  
 Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
                   435                  440                  445

<210> 16  
 <211> 446  
 <212> PRT  
 <213> Oryza sativa strain IR64

<400> 16

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
                   20                  25                  30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
                   35                  40                  45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
                   50                  55                  60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
 65                  70                  75                  80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
                   85                  90                  95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
                   100                  105                  110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
                   115                  120                  125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
                   130                  135                  140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val

206720 24062007

145		150		155		160
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	165		170		175	
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	180		185		190	
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	195		200		205	
Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	210		215		220	
Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	225		230		235	240
Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	245		250		255	
Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	260		265		270	
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	275		280		285	
Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro	290		295		300	
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	305		310		315	320
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	325		330		335	
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	340		345		350	
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	355		360		365	
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	370		375		380	



Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
 385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
 405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
 420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

<210> 17  
 <211> 2432  
 <212> DNA  
 <213> Oryza sativa cv. Kasalath

<220>  
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 <222> (1950)..(1950)  
 <223> N = G or C

<220>  
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 <223> N = G or C

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 acgtgccgga tcatttgcgc ttgcctgttg gttttgatcg gatctgttg ttgtgcgtgt 180  
 gtgatttggg gatcgacgt gcggggaagc taacctttgc atggataact tgagatttgt 240  
 gaggccgcgc ttcgaccaga tcggtcgcca atcttttagt ggctgaccgt ggaaagagga 300  
 tattactgac cttcggtttg ctaatttttg ttgtgccgtt gaatctgaaa taaccagaat 360  
 agtcatgggg aaaaaagtct gatctggaag gttcgaatta catttctata tattgttgtg 420  
 ctcccagacg atggttgcaa gaaattactc atgctggata aaattgtgga tgtaagagtc 480  
 tgcagttggt aaaatctgga aacagcacat tttgccgtag taaatttgaa tccatgttgc 540  
 tgtctcgtta ttggtgtgtt acgagtaacc tgtgtgttgt tatctccgt tggactagat 600  
 tocaagtaat ccagtgccct catgacctgc aaattctatg cctatgaagt aacatgaaca 660

gtttgtatgt attctgttga tgcatacttg cattatattgt gagatgtaca tgttgtggta 720  
aaatthttgca ttcaccatat agaaatagta actgactatc cttgttttagt tcgaaaacta 780  
ctgcaggthtt agttattctc tgttgccaag agtgcttggt atgattgtaa gggttacagt 840  
tctgtgacta accatgtaac aaatatatta aggattatca aattattcta tgtgaagtgt 900  
ccgtgcccta attgtgttat cttctgtaac tgatagcaca acatttgthtt cctgctgtgt 960  
gcttgtgtaa attggtactt catcattact atatatthtca aagaaaattc tgcattgcat 1020  
tcccgtcgtc cgttctaaat cagaactgac gattgctctg gtggctgaag ctccagaaag 1080  
aaagggaaaa ggccgaaaag aagaaagaga aaaggagtga caggaaagct cttccacatg 1140  
gtgagatata caagcattca aagcgaacct acaagaagag aaaacatgaa gacatcaata 1200  
atgctgatca gaagthcccg aaggtthtct ccatggaacc tggtgagcaa ttggagaaga 1260  
gtggactctc agaagagcat ggagctcctt gctthtactca gacagtgcatt ggctctccag 1320  
agagthtaca ggacagcagc aagagaagaa aggttggtgt acccagthct agccaagcta 1380  
agaatggtga ggccctthtct tgcatttgct thctthttagc tggtgatgtt gaattggthtt 1440  
gacttatctt gaattatcat cttgcaggta acatctthct aataaagata agaagagatc 1500  
aagattcttc agctthccct tccgagaaat ctaatgttgt acaaacacca gthcatcaaa 1560  
tgggatcagt thcatctctg ccaagtaaga aaaactcaat gcaaccacac aacaccgaaa 1620  
tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatthtt caagcagthc 1680  
tgaaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt cctccatcta 1740  
tgagggcatc aaaggaaagg gttggccttc gtcctgcaga gatgttggtc aatgttggtc 1800  
cttccacctc caaggcaaaa cagattgtca atctgcagc tgctaaggth acacaaagag 1860  
thgatctctc acctgccaag gcatctcaga gaattgatcc tctgttgcca tccaaggthc 1920  
atatagatgc tactcgatct thtacgaagn tctcccagac agagatcaag ccggaagthc 1980  
agcccccaat tccgaaggth cctgtggcta tgcctacct caatcgthcag cngattgaca 2040  
cctgcagacc caaagaagag ccttgctcct ctggcaggaa tgctgaagct gcttcagthc 2100  
cagtagagaa gcagthcaa gcagatgca aaaagagccg caaggctgag aagaaagaga 2160  
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atcttgggga ccaggatthg ctgcttggtg gtacgaggaa acctgatgct ggcattggca 2280  
actgcagaga aattgttgat ccacttactt ctcaatcagc agagcagthc tcatthcagc 2340

ctagggcgat tcatttacca gaccttcacg tctatcagtt gccatatgtg gttccattct 2400  
 aggtttgtgt agtgagatgg agtaggtgag aa 2432

<210> 18  
 <211> 1341  
 <212> DNA  
 <213> Oryza sativa cv. Kasalath

<220>  
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 <223>

<220>  
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 <222> (889)..(889)  
 <223> n = G, C

<220>  
 <221> misc\_feature  
 <222> (971)..(971)  
 <223> n = A, T

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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96  
 Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144  
 Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
 35 40 45

aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192  
 Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
 50 55 60

aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240  
 Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
 65 70 75 80

aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288  
 Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
 85 90 95

tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336  
 Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
 100 105 110

cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc	384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga	432
Ser Pro Ser Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta	480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag	528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca	576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa	624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	
195 200 205	
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct	672
Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro	
210 215 220	
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag	720
Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu	
225 230 235 240	
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc	768
Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val	
245 250 255	
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc	816
Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala	
260 265 270	
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata	864
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	
275 280 285	
gat gct act cga tct ttt acg aag ntc tcc cag aca gag atc aag ccg	912
Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro	
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	
305 310 315 320	
aat cgt cag cng att gac acc tcg cag ccc aaa gaa gag cct tgc tcc	1008
Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	
325 330 335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc	1056

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	
340 345 350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag	1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	
355 360 365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat	1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	
370 375 380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa	1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys	
385 390 395 400	
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act	1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr	
405 410 415	
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta	1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu	
420 425 430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	

<210> 19  
 <211> 446  
 <212> PRT  
 <213> Oryza sativa cv. Kasalath

<220>  
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 <222> (297)..(297)  
 <223> The 'Xaa' at location 297 stands for Ile, Val, Leu, or Phe.

<220>  
 <221> misc\_feature  
 <222> (324)..(324)  
 <223> The 'Xaa' at location 324 stands for Gln, Arg, Pro, or Leu.

<220>  
 <221> misc\_feature  
 <222> (889)..(889)  
 <223> n = G, C

<220>  
 <221> misc\_feature  
 <222> (971)..(971)  
 <223> n = A, T

<400> 19

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

206T20" 24054001

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
 245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
 260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
 275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Xaa Ser Gln Thr Glu Ile Lys Pro  
 290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
 305 310 315 320

Asn Arg Gln Xaa Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
 340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
 355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
 370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
 385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
 405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
 420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

- <210> 20
- <211> 2447
- <212> DNA
- <213> Oryza rufipogon strain 5948

<400> 20  
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gctcttgctt gttggttttg atcggatctg ttggttggtc gtgtgtgatt tggggatcgc 180  
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cagatcggtc gccaatcttt tagtggtga ccgtggaaag aggatattac tgaccttcgg 300  
tttgctaatt ttggttggtc cgttgaatct gaaataacca gaatagtcac ggggaaaaag 360  
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caagaaatta ctcatgctgg ataaaattgt ggatgtaaga gtctgcagtt gttaaaatct 480  
ggaaacagca cattttgccg tagtaaattt gaatccatgt tgctgtctcg ttattggtgt 540  
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tgatgcatac ttgcattatt tgtgagatgt acatgttggt gtaaaatttt gcattcacca 720  
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aacaatatata ttaaggatta tcaaattatt ctatgtgaag tgtccgtgcc ctaattgtgt 900  
tatcttctgt aactgatagc acaacatttg tttctgctg tgtgcttggt taaattggta 960  
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aatcagaact gacgattgct ctggtggctg aagctccaga aagaaagggg aaaggccgaa 1080  
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206120"24054001

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<210> 21
<211> 1341
<212> DNA
<213> Oryza rufipogon strain 5948

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<220>
<221> CDS
<222> (1)..(1341)
<223>

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<220>
<221> misc_feature
<222> (1)..(15)
<223> n = A, C, G, T

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Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln
20 25 30

aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg 144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg
35 40 45

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aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60	192
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80	240
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95	288
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser 100 105 110	336
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro 115 120 125	384
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg 130 135 140	432
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val 145 150 155 160	480
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys 165 170 175	528
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala 180 185 190	576
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys 195 200 205	624
caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca ccc tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816

aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata	864
Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile	
275 280 285	
gat gct act cga tct ttt acg aag ctc tcc cag aca gag atc aag ccg	912
Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro	
290 295 300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc	960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile	
305 310 315 320	
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc	1008
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser	
325 330 335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc	1056
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser	
340 345 350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag	1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys	
355 360 365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat	1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp	
370 375 380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa	1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys	
385 390 395 400	
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act	1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr	
405 410 415	
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta	1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu	
420 425 430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	

<210> 22  
 <211> 446  
 <212> PRT  
 <213> Oryza rufipogon strain 5948

<220>  
 <221> misc\_feature  
 <222> (1)..(1)  
 <223> The 'Xaa' at location 1 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (2)..(2)  
 <223> The 'Xaa' at location 2 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (3)..(3)  
 <223> The 'Xaa' at location 3 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (4)..(4)  
 <223> The 'Xaa' at location 4 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (5)..(5)  
 <223> The 'Xaa' at location 5 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (1)..(15)  
 <223> n = A, C, G, T

<400> 22

Xaa Xaa Xaa Xaa Xaa Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
 1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg  
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
 50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
 65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
 85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro  
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
305 310 315 320

205420 2405400T

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
420 425 430

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 23  
<211> 146  
<212> DNA  
<213> Oryza rufipogon strain 5949

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cgaggtgctt cccctacccg ccgcccgggt acgtgcgaaa ccagtggtg gccgtggccg 120  
cggccgaagc gcaggcgacc actaag 146

<210> 24  
<211> 1615  
<212> DNA  
<213> Oryza rufipogon strain 5949

<400> 24  
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ccgtgcccta atttgtttat cttctgtaac tgatagcaca acatttggtt cctgctgtgt 120  
gcttgtgtaa attggtactt catcattact atatatttca aagaaaattc tgcattgcat 180

tcccgtcgtc cgttctaaat cagaactgac gattgctctg gtggctgaag ctccagaaag	240
aaagggaaaa ggccgaaaag aagaaagaga aaaagagtga caggaaagct cttccacatg	300
gtgagatata caagcattca aagcgaaccc acaagaagag aaaacatgaa gacatcaata	360
atgctgatca gaagtcccg aaggtttcct ccatggaacc tggtagcaa ttggagaaga	420
gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac ggctctccag	480
agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtcct agccaagcta	540
agaatggatga ggccctttct tgcatttgct ttctcttagc tggtagatgtt gaattggttt	600
gacttatcct gaattatcat cttgcaggta acatccttgc aataaagata agaagagatc	660
aagattcttc agcttccctt tcggagaaat ctaatgttgt acaaacacca gttcatcaaa	720
tgggatcagt ttcattctctg ccaagtaaga aaaactcaat gcaaccacac aacaccgaaa	780
tgatggatga aacagcatca acccagcagc aaagcatcaa aggtgatgtt caagcagtac	840
tgaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt cctccatcta	900
tgagggcatc aaaggaaagg gttggccttc gtccctgcaga gatgttggtc aatgttggtc	960
cttcaccatc caaggcaaaa cagattgtca atcctgcagc tgctaagggtt acacaaagag	1020
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atatagatgc tactcgatct ttacgaagg tctccagac agagatcaag ccggaagtac	1140
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cctgcagacc caaagaagag ccttgctcct ctggcaggaa tgctgaagct gcttcagtat	1260
cagtagagaa gcagtccaag tcagatcgca aaaagagccg caaggctgag aagaaagaga	1320
agaagttcaa agatttatctt gttacctggg atcctccgtc tatggaaatg gatgatatgg	1380
atcttgggga ccaggattgg ctgcttggtg gtacgaggaa acctgatgct ggcattggca	1440
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ctagggcgat tcatttacca gaccttcagc tctatcagtt gccatatgtg gttccattct	1560
aggtttgtgt agtgagatgg agtaggtgag aagtagagag atgttgggag agagc	1615

<210> 25  
 <211> 1341  
 <212> DNA  
 <213> Oryza rufipogon strain 5949

<220>  
 <221> CDS

<222> (1)..(1341)

<223>

<400> 25

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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag	96
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln	
20 25 30	
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg	144
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg	
35 40 45	
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac	192
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His	
50 55 60	
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg	240
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg	
65 70 75 80	
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc	288
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu	
85 90 95	
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct	336
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser	
100 105 110	
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc	384
Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro	
115 120 125	
agt cct agc caa gct aag aat ggt aac atc ctt cga ata aag ata aga	432
Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg	
130 135 140	
aga gat caa gat tct tca gct tcc ctt tcg gag aaa tct aat gtt gta	480
Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val	
145 150 155 160	
caa aca cca gtt cat caa atg gga tca gtt tca tct ctg cca agt aag	528
Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys	
165 170 175	
aaa aac tca atg caa cca cac aac acc gaa atg atg gtg aga aca gca	576
Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala	
180 185 190	
tca acc cag cag caa agc atc aaa ggt gat ttt caa gca gta ctg aaa	624
Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys	
195 200 205	



caa ggt atg cca acc cca gca aaa gtc atg cca aga gtc gat gtt cct Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro 210 215 220	672
cca tct atg agg gca tca aag gaa agg gtt ggc ctt cgt cct gca gag Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu 225 230 235 240	720
atg ttg gcc aat gtt ggt cct tca cca tcc aag gca aaa cag att gtc Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val 245 250 255	768
aat cct gca gct gct aag gtt aca caa aga gtt gat cct cca cct gcc Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala 260 265 270	816
aag gca tct cag aga att gat cct ctg ttg cca tcc aag gtt cat ata Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile 275 280 285	864
gat gct act cga tct ttt acg aag gtc tcc cag aca gag atc aag ccg Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro 290 295 300	912
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile 305 310 315 320	960
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser 325 330 335	1008
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser 340 345 350	1056
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys 355 360 365	1104
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp 370 375 380	1152
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400	1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415	1248
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430	1296
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag	1341

Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

<210> 26  
 <211> 446  
 <212> PRT  
 <213> Oryza rufipogon strain 5949

<400> 26

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
 1 5 10 15

Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30

Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg  
 35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
 50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
 65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
 85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
 100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
 115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
 130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
 145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
 165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
 180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
 195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
 210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
 225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
 245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
 260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
 275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro  
 290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
 305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
 340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
 355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
 370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
 385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
 405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
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Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
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 gacatcaata atgctgatca gaagtcccg aaggtttcct ccatggaacc tggtagacaa 180  
 ttggagaaga gtggactctc agaagagcat ggagctcctt gctttactca gacagtgcac 240  
 ggctctccag agagttcaca ggacagcagc aagagaagaa aggttgtgtt acccagtcct 300  
 agccaagcta agaatggtga ggccctttct tgcatttttc ttcttttagc tggtagatgtt 360  
 gaattgggtt gacttatect gaattatcat cttgcaggta acatccttcg aataaagata 420  
 agaagagatc aagattcttc agcttccctt tcggagaaat ctaatgttgt acaaacacca 480  
 gttcatcaaa tgggatcagt ttcattctctg ccaagtaaga aaaactcaat gcaaccacac 540  
 aacaccgaaa tgatggtgag aacagcatca acccagcagc aaagcatcaa aggtgatattt 600  
 caagcagtac tgaaacaagg tatgccaacc ccagcaaaag tcatgccaag agtcgatgtt 660  
 cctccatcta tgagggcatc aaaggaaagg gttggccttc gtctgcaga gatgttggcc 720  
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 ccggaagtac agccccaat tccgaagggtg cctgtggcta tgcctaccat caatcgtcag 960

cagattgaca cctcgcagcc caaagaagag ccttgctcct ctggcaggaa tgctgaagct 1020  
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aagaaagaga agaagttcaa agattttattt gttacctggg atcctccgtc tatggaaatg 1140  
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
20 25 30  
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144  
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg  
35 40 45  
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192  
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
50 55 60  
aag aag aga aaa cat gaa gac atc aat aat gct gat cag aag tcc cgg 240  
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
65 70 75 80  
aag gtt tcc tcc atg gaa cct ggt gag caa ttg gag aag agt gga ctc 288  
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
85 90 95  
tca gaa gag cat gga gct cct tgc ttt act cag aca gtg cat ggc tct 336  
Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
100 105 110  
cca gag agt tca cag gac agc agc aag aga aga aag gtt gtg tta ccc 384

Pro	Glu	Ser	Ser	Gln	Asp	Ser	Ser	Lys	Arg	Arg	Lys	Val	Val	Leu	Pro		
		115					120					125					
agt	cct	agc	caa	gct	aag	aat	ggt	aac	atc	ctt	cga	ata	aag	ata	aga		432
Ser	Pro	Ser	Gln	Ala	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Ile	Lys	Ile	Arg		
	130					135				140							
aga	gat	caa	gat	tct	tca	gct	tcc	ctt	tcg	gag	aaa	tct	aat	gtt	gta		480
Arg	Asp	Gln	Asp	Ser	Ser	Ala	Ser	Leu	Ser	Glu	Lys	Ser	Asn	Val	Val		
	145				150					155					160		
caa	aca	cca	gtt	cat	caa	atg	gga	tca	gtt	tca	tct	ctg	cca	agt	aag		528
Gln	Thr	Pro	Val	His	Gln	Met	Gly	Ser	Val	Ser	Ser	Leu	Pro	Ser	Lys		
				165					170						175		
aaa	aac	tca	atg	caa	cca	cac	aac	acc	gaa	atg	atg	gtg	aga	aca	gca		576
Lys	Asn	Ser	Met	Gln	Pro	His	Asn	Thr	Glu	Met	Met	Val	Arg	Thr	Ala		
			180					185					190				
tca	acc	cag	cag	caa	agc	atc	aaa	ggt	gat	ttt	caa	gca	gta	ctg	aaa		624
Ser	Thr	Gln	Gln	Gln	Ser	Ile	Lys	Gly	Asp	Phe	Gln	Ala	Val	Leu	Lys		
		195					200					205					
caa	ggt	atg	cca	acc	cca	gca	aaa	gtc	atg	cca	aga	gtc	gat	gtt	cct		672
Gln	Gly	Met	Pro	Thr	Pro	Ala	Lys	Val	Met	Pro	Arg	Val	Asp	Val	Pro		
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cca	tct	atg	agg	gca	tca	aag	gaa	agg	gtt	ggc	ctt	cgt	cct	gca	gag		720
Pro	Ser	Met	Arg	Ala	Ser	Lys	Glu	Arg	Val	Gly	Leu	Arg	Pro	Ala	Glu		
	225				230				235						240		
atg	ttg	gcc	aat	gtt	ggt	cct	tca	ccc	tcc	aag	gca	aaa	cag	att	gtc		768
Met	Leu	Ala	Asn	Val	Gly	Pro	Ser	Pro	Ser	Lys	Ala	Lys	Gln	Ile	Val		
				245					250						255		
aat	cct	gca	gct	gct	aag	gtt	aca	caa	aga	gtt	gat	cct	cca	cct	gcc		816
Asn	Pro	Ala	Ala	Ala	Lys	Val	Thr	Gln	Arg	Val	Asp	Pro	Pro	Pro	Ala		
			260					265					270				
aag	gca	tct	cag	aga	att	gat	cct	ctg	ttg	cca	tcc	aag	gtt	cat	ata		864
Lys	Ala	Ser	Gln	Arg	Ile	Asp	Pro	Leu	Leu	Pro	Ser	Lys	Val	His	Ile		
		275					280						285				
gat	gct	act	cga	tct	ttt	acg	aag	ctc	tcc	cag	aca	gag	atc	aag	ccg		912
Asp	Ala	Thr	Arg	Ser	Phe	Thr	Lys	Leu	Ser	Gln	Thr	Glu	Ile	Lys	Pro		
	290					295					300						
gaa	gta	cag	ccc	cca	att	ccg	aag	gtg	cct	gtg	gct	atg	cct	acc	atc		960
Glu	Val	Gln	Pro	Pro	Ile	Pro	Lys	Val	Pro	Val	Ala	Met	Pro	Thr	Ile		
	305				310					315					320		
aat	cgt	cag	cag	att	gac	acc	tcg	cag	ccc	aaa	gaa	gag	cct	tgc	tcc		1008
Asn	Arg	Gln	Gln	Ile	Asp	Thr	Ser	Gln	Pro	Lys	Glu	Glu	Pro	Cys	Ser		
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Ser	Gly	Arg	Asn	Ala	Glu	Ala	Ala	Ser	Val	Ser	Val	Glu	Lys	Gln	Ser		

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gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys 385 390 395 400			1200
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr 405 410 415			1248
tct caa tca gcg gag cag ttc tca ttg cag cct agg gcg att cat tta Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu 420 425 430			1296
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Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg 35 40 45			
Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His 50 55 60			
Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg 65 70 75 80			
Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu 85 90 95			

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
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Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
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Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
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Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Leu Ser Gln Thr Glu Ile Lys Pro  
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
305 310 315 320



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Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
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Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
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Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
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gtg gtg gcc gtg gcc gcg gcc gaa gcg cag gcg acc act aag ctc cag 96  
Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
20 25 30  
aaa gaa agg gaa aag gcc gaa aag aag aaa gag aaa aag agt gac agg 144  
Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg  
35 40 45  
aaa gct ctt cca cat ggt gag ata tcc aag cat tca aag cga acc cac 192

Lys	Ala	Leu	Pro	His	Gly	Glu	Ile	Ser	Lys	His	Ser	Lys	Arg	Thr	His		
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Lys	Lys	Arg	Lys	His	Glu	Asp	Ile	Asn	Asn	Ala	Asp	Gln	Lys	Ser	Arg		
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aag	gtt	tcc	tcc	atg	gaa	cct	ggt	gag	caa	ttg	gag	aag	agt	gga	ctc	288	
Lys	Val	Ser	Ser	Met	Glu	Pro	Gly	Glu	Gln	Leu	Glu	Lys	Ser	Gly	Leu		
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tca	gaa	gag	cat	gga	gct	cct	tgc	ttt	act	cag	aca	gtg	cat	ggc	tct	336	
Ser	Glu	Glu	His	Gly	Ala	Pro	Cys	Phe	Thr	Gln	Thr	Val	His	Gly	Ser		
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Pro	Glu	Ser	Ser	Gln	Asp	Ser	Ser	Lys	Arg	Arg	Lys	Val	Val	Leu	Pro		
		115					120					125					
agt	cct	agc	caa	gct	aag	aat	ggt	aac	atc	ctt	cga	ata	aag	ata	aga	432	
Ser	Pro	Ser	Gln	Ala	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Ile	Lys	Ile	Arg		
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Arg	Asp	Gln	Asp	Ser	Ser	Ala	Ser	Leu	Ser	Glu	Lys	Ser	Asn	Val	Val		
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Gln	Thr	Pro	Val	His	Gln	Met	Gly	Ser	Val	Ser	Ser	Leu	Pro	Ser	Lys		
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Lys	Asn	Ser	Met	Gln	Pro	His	Asn	Thr	Glu	Met	Met	Val	Arg	Thr	Ala		
			180					185						190			
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Ser	Thr	Gln	Gln	Gln	Ser	Ile	Lys	Gly	Asp	Phe	Gln	Ala	Val	Leu	Lys		
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Gln	Gly	Met	Pro	Thr	Pro	Ala	Lys	Val	Met	Pro	Arg	Val	Asp	Val	Pro		
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cca	tct	atg	agg	gca	tca	aag	gaa	agg	gtt	ggc	ctt	cgt	cct	gca	gag	720	
Pro	Ser	Met	Arg	Ala	Ser	Lys	Glu	Arg	Val	Gly	Leu	Arg	Pro	Ala	Glu		
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Met	Leu	Ala	Asn	Val	Gly	Pro	Ser	Pro	Ser	Lys	Ala	Lys	Gln	Ile	Val		
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Asn	Pro	Ala	Ala	Ala	Lys	Val	Thr	Gln	Arg	Val	Asp	Pro	Pro	Pro	Ala		
			260					265					270				
aag	gca	tct	cag	aga	att	gat	cct	ctg	ttg	cca	tcc	aag	gtt	cat	ata	864	
Lys	Ala	Ser	Gln	Arg	Ile	Asp	Pro	Leu	Leu	Pro	Ser	Lys	Val	His	Ile		

20050401 24052001

275	280	285	
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290	295	300	
gaa gta cag ccc cca att ccg aag gtg cct gtg gct atg cct acc atc			960
Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile			
305	310	315	320
aat cgt cag cag att gac acc tcg cag ccc aaa gaa gag cct tgc tcc			1008
Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser			
325	330	335	
tct ggc agg aat gct gaa gct gct tca gta tca gta gag aag cag tcc			1056
Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser			
340	345	350	
aag tca gat cgc aaa aag agc cgc aag gct gag aag aaa gag aag aag			1104
Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys			
355	360	365	
ttc aaa gat tta ttt gtt acc tgg gat cct ccg tct atg gaa atg gat			1152
Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp			
370	375	380	
gat atg gat ctt ggg gac cag gat tgg ctg ctt ggt agt acg agg aaa			1200
Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys			
385	390	395	400
cct gat gct ggc att ggc aac tgc aga gaa att gtt gat cca ctt act			1248
Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr			
405	410	415	
tct caa tca gca gag cag ttc tca ttg cag cct agg gcg att cat tta			1296
Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu			
420	425	430	
cca gac ctt cat gtc tat cag ttg cca tat gtg gtt cca ttc tag			1341
Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe			
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Val Val Ala Val Ala Ala Ala Glu Ala Gln Ala Thr Thr Lys Leu Gln  
 20 25 30

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Lys Glu Arg Glu Lys Ala Glu Lys Lys Lys Glu Lys Lys Ser Asp Arg  
35 40 45

Lys Ala Leu Pro His Gly Glu Ile Ser Lys His Ser Lys Arg Thr His  
50 55 60

Lys Lys Arg Lys His Glu Asp Ile Asn Asn Ala Asp Gln Lys Ser Arg  
65 70 75 80

Lys Val Ser Ser Met Glu Pro Gly Glu Gln Leu Glu Lys Ser Gly Leu  
85 90 95

Ser Glu Glu His Gly Ala Pro Cys Phe Thr Gln Thr Val His Gly Ser  
100 105 110

Pro Glu Ser Ser Gln Asp Ser Ser Lys Arg Arg Lys Val Val Leu Pro  
115 120 125

Ser Pro Ser Gln Ala Lys Asn Gly Asn Ile Leu Arg Ile Lys Ile Arg  
130 135 140

Arg Asp Gln Asp Ser Ser Ala Ser Leu Ser Glu Lys Ser Asn Val Val  
145 150 155 160

Gln Thr Pro Val His Gln Met Gly Ser Val Ser Ser Leu Pro Ser Lys  
165 170 175

Lys Asn Ser Met Gln Pro His Asn Thr Glu Met Met Val Arg Thr Ala  
180 185 190

Ser Thr Gln Gln Gln Ser Ile Lys Gly Asp Phe Gln Ala Val Leu Lys  
195 200 205

Gln Gly Met Pro Thr Pro Ala Lys Val Met Pro Arg Val Asp Val Pro  
210 215 220

Pro Ser Met Arg Ala Ser Lys Glu Arg Val Gly Leu Arg Pro Ala Glu  
225 230 235 240

Met Leu Ala Asn Val Gly Pro Ser Pro Ser Lys Ala Lys Gln Ile Val  
245 250 255

Asn Pro Ala Ala Ala Lys Val Thr Gln Arg Val Asp Pro Pro Pro Ala  
260 265 270

Lys Ala Ser Gln Arg Ile Asp Pro Leu Leu Pro Ser Lys Val His Ile  
275 280 285

Asp Ala Thr Arg Ser Phe Thr Lys Val Ser Gln Thr Glu Ile Lys Pro  
290 295 300

Glu Val Gln Pro Pro Ile Pro Lys Val Pro Val Ala Met Pro Thr Ile  
305 310 315 320

Asn Arg Gln Gln Ile Asp Thr Ser Gln Pro Lys Glu Glu Pro Cys Ser  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Ala Ser Val Ser Val Glu Lys Gln Ser  
340 345 350

Lys Ser Asp Arg Lys Lys Ser Arg Lys Ala Glu Lys Lys Glu Lys Lys  
355 360 365

Phe Lys Asp Leu Phe Val Thr Trp Asp Pro Pro Ser Met Glu Met Asp  
370 375 380

Asp Met Asp Leu Gly Asp Gln Asp Trp Leu Leu Gly Ser Thr Arg Lys  
385 390 395 400

Pro Asp Ala Gly Ile Gly Asn Cys Arg Glu Ile Val Asp Pro Leu Thr  
405 410 415

Ser Gln Ser Ala Glu Gln Phe Ser Leu Gln Pro Arg Ala Ile His Leu  
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Pro Asp Leu His Val Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 33

<211> 180

<212> DNA

<213> Zea mays mays strain BS7

<400> 33

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gatcgtttgt tcaatctgta ggttttgcgc ggatctgtgt gtttgcgcgt gcgtgatgtg 180

<210> 34

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<213> Zea mays mays strain BS7

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aaagcacagc cataagaaga gaaagcttga agatgtcatc aaagctgagc aggggtcccaa 180

aagagtaccc aaagaatcag ttgagcagtt ggagaagagt ggactctcag aagagcatgg 240

agctccttct tttgtacata cgatacgtga ctctcctgag agctcacagg acagcggcaa 300

gagacgaaaag gttgtcctgt ccagtcctag ccaacctaaag aatgggtgaga ctattctctt 360

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gayccccaat cagctgttct ggagaaacca agggttcttg agcaaccatt ggtccaacaa 540

atgggatcag gttcatcccy gtcgggcaag caaaattcaa tccatcataa gatgaatgtg 600

agatctacct ctggtcagcg gagggctgat ggtgactccc aagcagtaca aaaatgtttg 660

attacagaat ccccggc aaa gaccatgcag agacttgtcc cccagcctgc agctaaggtc 720

acacatcctg ttgatcccca gtcagctggt aagggtgccag ttggaagatc gggcctacct 780

ctgaagtctt cggaagtgt ggacccttcg cctgctagag ttatgagaag atttgatcct 840

ccacctgtta agatgatgtc acagagagtt caccatccag cttccatggg gtcgcagaaa 900

gttgatcctc cgtttccgaa ggtattacat aaggaaaccg gatctgttgt tcgcctacca 960

gaagctaccc ggcctactgt tcttcaaaaa cccaaggact tgcttgctat caagcagcag 1020

gatatcagga cctcttctc aaaagaagag ccctgcttct ctggtaggaa tgcagaagca 1080

gttcaagtgc aagatactaa gctctcccgg tcagacatga agaaaatccg caaagctgag 1140

aaaaaagata agaagttcag agatctgttt gttacctgga atccggtatt gatagagaat 1200

gaaggttcag atcttggtga tgaagactgg ctgttcagca gtaaaaggaa ctccgatgct 1260

atcatggttc aaagcagagc tactgatagt tcagtgccga tccatccaat ggtgcagcag 1320

aagccttctt tacaaccag ggcaacattt ttgccggacc ttaatatgta ccagctgcca 1380

tatgtcgtac cattttaaac atctggcgag gtagatgaga attagatgag atgttgggag 1440

agagctg

1447

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 <213> Zea mays mays strain BS7

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 atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48  
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 1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96  
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
 20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
 35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384  
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
 115 120 125

cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gay 432  
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
 130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480  
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
 145 150 155 160

gtc caa caa atg gga tca ggt tca tcc cyg tcg ggc aag caa aat tca 528

Val Gln Gln Met Gly Ser Gly Ser Ser Xaa Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga	768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc	1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe	
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc	1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	
340 345 350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag	1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	
355 360 365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	
370 375 380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac	1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	



385	390	395	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg				1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro				
405	410	415		
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca				1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr				
420	425	430		
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt				1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe				
435	440	445		
taa				1347

<210> 36  
 <211> 448  
 <212> PRT  
 <213> Zea mays mays strain BS7  
  
 <220>  
 <221> misc\_feature  
 <222> (170)..(170)  
 <223> The 'Xaa' at location 170 stands for Pro, or Leu.

<400> 36

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro				
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys				
20	25	30		
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro				
35	40	45		
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg				
50	55	60		
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro				
65	70	75	80	
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His				
85	90	95		
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser				
100	105	110		

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Xaa Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser

205 F 230 2406400T

340

345

350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 37

<211> 2646

<212> DNA

<213> Zea mays mays strain HuoBai

<400> 37

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ttcggattta cacacgcacg tgccagatcg tttgttcaat ctgtaggttt tgcgcggatc	180
tgtggtttgc gcgtgcgtga tgtgggtatt gcccgtcct tgaaagctaa ccgagctgag	240
gaagtgtatg gatccttgtgt agctgcacga ggtcctccaa atcgattgta aaatttaagt	300
tgtatggccg gtaggccaag attgggttat tccggttttc gaaaactggg agcatgggta	360
tcggggacat tgaaagaatg gtagaacatc aaattcgatt caaaactgtg ctagatttgc	420
atatttagtc gccctaaaat tacgtggacg tgggtgatcc gaattggttg ttgtatgatg	480
gttgggaagtg actggccaaa tttttttgtt tctcaaagtt ttctttgaaa aactgtttgt	540
cgagcgtcaa ttcgtattta cctgaattta ctaattctta atacagtatg tcgttatttt	600
gggctaagct tgtgtaagaa gggtcgtttg acattttgta ctgtattgat gctgttttgt	660
gtttctttgt tcggagcagc attcaatgct ctttttggtg tttgagagaa tctgatattt	720

gccatcgtag cgaaagtcg aaaccaacta ttcaaattgg gatttcattt cttttttttt	780
ctactgtttt tagagttctc tttttcgctg ctgtgctctt gtgggtcagt acgtgcattt	840
ctcttttttt cttttttttt ctgatgttac tcttctgttg accaaaggag ttcagaatta	900
ttttggccct gtatatcaat agcaaccaac accatttatt gagcccattt ttagttttct	960
tgttctgtag agtatgcatt gttgcaggtc ttaactgttg tcagggaggt aacgtgttca	1020
acatgattgt aaacgaatac aattctgttg ctaactgtgt aatgatgaga aggataattg	1080
aataatcttt gtgaagtatt actgtctgaa ctgtacgcaa atgctacatt tattctttgt	1140
gttcgtgtaa atatcattat acataaaaaat gctgcattgc attcccgtcg tccgttctaa	1200
atcagaactg acgattgctc tgggtggctga agctcctgaa agaaaaggaa aaggccgaaa	1260
agaagaaaga gaaaaggagt gacaggaaag ctcccaagca gtgtgagacg tccaaacatt	1320
caaagcacag ccataagaag agaaagcttg aagatgtcat caaagctgag cagggtccca	1380
aaagagtacc caaagaatca gttgagcagt tggagaagag tggactctca gaagagcatg	1440
gagctccttc ttttgtacat acgatacgtg actctcctga gagctcacag gacagcggca	1500
agagacgaaa ggttgtcctg tccagtcta gccaacctaa gaatggtgag actattctct	1560
tgtttttgct attctgattg attttttatt atagaagaaa tcaatatctt gttcaggatt	1620
ttattcatcc caacttgatt ttacaggaaa cattcttcgc ttcaagatta aaagtagtca	1680
agatcccca ttagctgttc tggagaaacc aagggttctt gagcaaccat tggccaaca	1740
aatgggatca ggttcatccc tgtcgggcaa gcaaaattca atccatcata agatgaatgt	1800
gagatctacc tctggtcagc ggaggggtcaa tgggtgactcc caagcagtag aaaaatgttt	1860
gattacagaa tccccggcaa agaccatgca gagacttgct cccagcctg cagctaaggt	1920
cacacatcct gttgatcccc agtcagctgt taagggtgcca gttggaagat cgggcctacc	1980
tctgaagtct tcgggaagtg tggacccttc gcctgctaga gttatgagaa gatttgatcc	2040
tccacctgtt aagatgatgt cacagagagt tcaccatcca gttccatgg tgtcgcagaa	2100
agttgatcct ccgtttccga aggtattaca taaggaaacc ggatctgttg ttcgcctacc	2160
agaagctacc cggcctactg ttcttcaaaa acccaaggac ttgcctgcta tcaagcagca	2220
ggatatcagg acctcttctt caaaagaaga gccctgcttc tctggtagga atgcagaagc	2280
agttcaagtg caagatacta agctctcccg gtcagacatg aagaaaatcc gcaaagctga	2340
gaaaaaagat aagaagttca gagatctgtt tgttacctgg aatccggtat tgatagagaa	2400
tgaaggttca gatcttggtg atgaagactg gctgttcagc agtaaaagga actccgatgc	2460

tatcatgggtt caaagcagag ctactgatag ttcagtgccg atccatccaa tgggtgcagca 2520  
gaagccttctt ttacaaccca gggcaacatt tttgccggac cttaatatgt accagctgcc 2580  
atatgtcgta ccattttaaa catctggcga ggtagatgag aattagatga gatgttggga 2640  
gagagc 2646

<210> 38  
<211> 1347  
<212> DNA  
<213> Zea mays mays strain HuoBai

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<400> 38  
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48  
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1 5 10 15  
gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96  
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
20 25 30  
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45  
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
50 55 60  
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80  
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95  
gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110  
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384  
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125  
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432  
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350	1056
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365	1104

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	
370 375 380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac	1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	
385 390 395 400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg	1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	
405 410 415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca	1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	
420 425 430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt	1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	
taa	1347
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<212> PRT	
<213> Zea mays mays strain HuoBai	
<400> 39	
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys	
20 25 30	
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro	
35 40 45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg	
50 55 60	
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro	
65 70 75 80	
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His	
85 90 95	
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser	
100 105 110	

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
 115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
 130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
 145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
 165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
 180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
 195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
 210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
 225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
 245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
 260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
 275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
 305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
 325 330 335



Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
 340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
 405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
 420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

<210> 40  
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 <212> DNA  
 <213> Zea mays mays strain Makki  
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 gagccggagt cgaccgctaa ggtttgttga accttcggat ttacacacgc acgtgccaga 180  
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 attgcccggtg ccttgaaagc ta 262

<210> 41  
 <211> 2311  
 <212> DNA  
 <213> Zea mays mays strain Makki  
 <400> 41  
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 gattcaaaac tgtgctagat ttgcatatct agtcgcccta aaattacgtg gacgtgggtg 120  
 atccgaattg gttgttgtat gatggttga agtgactggc caaatttttt tgtttctcaa 180

agttttcttt gacaaactgt ttgtcgagcg tcaattcgta tttacctgaa tttactaatt	240
cttaatacag tatgtcgta ttttgggcta agcttgtgta agaagggtcg tttgacattt	300
tgtactgtat tgatgctgtt ttgtgtttct ttgttcggag cagcattcaa tgctcctttt	360
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ttgggatttc atttcttttt ttttctactg tttttagagt tctctttttc gctgctgtgc	480
tcttgtgggt cagtacgtgc atttctcttt ttttcttttt ttttctgatg ttactcttct	540
gttgaccaa ggagttcaga attattttgg acctgtatat caatagcaac caacaccatt	600
tattgagccc atttttagtt ttcttgttct gtagagtatg cattgttgca ggtcttaact	660
gttgtcaggg aagtaacgtg ttcaacatga ttgtaaacga atacaattct gttgctaact	720
gtgtaatgat gagaaggata attgaataat ctttgtgaag tattactgtc tgaactgtac	780
gcaaattgcta cattcattct ttgtgttcgt gtaaataatca ttatacataa aaatgctgca	840
ttgcattccc gtcgtccgtt ctaaatacaga actgacgatt gctctgggtg ctgaagctcc	900
tgaaagaaaa ggaaaaggcc gaaaagaaga aagagaaaag gagtgacagg aaagctccca	960
agcagtgtga gacgtccaaa cattcaaagc acagccataa gaagagaaaag cttgaagatg	1020
tcatcaaagc tgagcaggggt cccaaaagag tacccaaaga atcagttgag cagttggaga	1080
agagtggact ctcagaagag catggagctc cttcttttgt acatacgata cgtgactctc	1140
ctgagagctc acaggacagc ggcaagagac gaaaggttgt cctgtccagt cctagccaac	1200
ctaagaatgg tgagactatt ctcttgtttt tgctattctg attgattttt tattatagaa	1260
gaaatcaatc gcttgttcag gattttattc atcccaactt gattttacag gaaacattct	1320
tcgcttcaag attaaaagta gtcaagatcc ccaatcagct gttctggaga aaccaagggt	1380
tcttgagcaa ccattggtec aacaaatggg atcaggttca tccctgtcgg gcaagcaaaa	1440
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ctcccaagca gtacaaaaat gtttgattac agaatccccg gcaaagacca tgcagagact	1560
tgtccccag cctgcagcta aggtcacaca tcctgttgat cccagtcag ctgttaaggt	1620
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tccagcttcc atgggtgtcg agaaagttga tcctccgttt ccgaaggat tacataagga	1800
aaccggatct gttgttcgcc taccagaagc taccggcct actgttcttc aaaaacccaa	1860
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cagcagtaaa aggaactccg atgctatcat ggttcaaagc agagctactg atagttcagt 2160
gccgatccat ccaatggtgc agcagaagcc ttctttacaa cccagggcaa catttttgcc 2220
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<210> 42
<211> 1347
<212> DNA
<213> Zea mays mays strain Makki

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<222> (1)..(1347)
<223>

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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

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Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln		
	115						120					125					
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gat	432	
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp		
	130					135					140						
ccc	caa	tca	gct	gtt	ctg	gag	aaa	cca	agg	gtt	ctt	gag	caa	cca	ttg	480	
Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu		
	145				150					155					160		
gtc	caa	caa	atg	gga	tca	ggg	tca	tcc	ctg	tcg	ggc	aag	caa	aat	tca	528	
Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Leu	Ser	Gly	Lys	Gln	Asn	Ser		
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atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggg	cag	cgg	agg	gtc	576	
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val		
			180					185					190				
aat	ggg	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg	624	
Asn	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro		
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Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr		
	210					215					220						
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His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser		
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ggc	cta	cct	ctg	aag	tct	tcg	gga	agt	gtg	gac	cct	tcg	cct	gct	aga	768	
Gly	Leu	Pro	Leu	Lys	Ser	Xaa	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg		
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gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga	816	
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg		
			260					265					270				
gtt	cac	cat	cca	gct	tcc	atg	gtg	tcg	cag	aaa	gtt	gat	cct	ccg	ttt	864	
Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe		
		275					280					285					
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa	912	
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu		
	290					295					300						
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc	960	
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile		
	305				310				315						320		
aag	cag	cag	gat	atc	agg	acc	tct	tcc	tca	aaa	gaa	gag	ccc	tgc	ttc	1008	
Lys	Gln	Gln	Asp	Ile	Arg	Thr	Ser	Ser	Ser	Lys	Glu	Glu	Pro	Cys	Phe		
			325						330					335			
tct	ggg	agg	aat	gca	gaa	gca	gtt	caa	gtg	caa	gat	act	aag	ctc	tcc	1056	
Ser	Gly	Arg	Asn	Ala	Glu	Ala	Val	Gln	Val	Gln	Asp	Thr	Lys	Leu	Ser		

340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag			1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys			
355	360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa			1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu			
370	375	380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac			1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn			
385	390	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg			1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro			
405	410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca			1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr			
420	425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt			1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe			
435	440	445	
taa			1347

<210> 43  
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 <212> PRT  
 <213> Zea mays mays strain Makki  
 <220>  
 <221> misc\_feature  
 <222> (247)..(247)  
 <223> The 'Xaa' at location 247 stands for Ser.  
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Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro	
35 40 45	
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg	
50 55 60	

1004042001

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Xaa Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
 305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
 340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
 370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
 385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
 405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
 420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

&lt;210&gt; 44

&lt;211&gt; 125

&lt;212&gt; DNA

&lt;213&gt; Zea mays mays strain Min13

&lt;400&gt; 44

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cctaccgcgc accgggggtac gtgcggaacc cagtggccgt ggccgagccg gattcgaccg 120

ctaag 125

&lt;210&gt; 45

&lt;211&gt; 198

&lt;212&gt; DNA

&lt;213&gt; Zea mays mays strain Min13

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 gttgtttgag agaatctgat atttgccatc gtaccgaaag tccgaaacca actattcaaa 180  
 ttgggatttc atttcttt 198

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 <213> Zea mays mays strain Min13

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 ttgttgcagg tcttaactgt tgtcagggaa gtaacgtgtt caacatgatt gtaaacgaat 180  
 acaattctgt tgctaactgt gtaatgatga gaaggataat tgaataatct ttgtgaagta 240  
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 atacataaaa atgctgcatt gcattcccgt cgtccgttct aaatcagaac tgacgattgc 360  
 tctgggtggct gaagctcctg aaagaaaagg aaaaggccga aaagaagaaa gagaaaagga 420  
 gtgacaggaa agtcccaaag cagtgtgaga cgtccaaaca ttcaaagcac agccataaga 480  
 agagaaagct tgaagatgtc atcaaagctg agcaggggtcc caaaagagta cccaaagaat 540  
 cagttgagca gttggagaag agtggactct cagaagagca tggagctcct tcttttgtac 600  
 atacgatacg tgactctcct gagagctcac aggacagcgg caagagacga aaggttgtcc 660  
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gaaggtatta cataaggaaa ccggatctgt tgttcgccta ccagaagcta cccggcctac 1320  
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 cagggcaaca tttttgccgg accttaatat gtaccagctg ccatatgtcg taccatttta 1740  
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 <212> DNA  
 <213> Zea mays mays strain Min13

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 <223>

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 gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96  
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
 20 25 30  
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
 35 40 45  
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
 50 55 60  
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80  
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95  
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336

Gly	Ala	Pro	Ser	Phe	Val	His	Thr	Ile	Arg	Asp	Ser	Pro	Glu	Ser	Ser		
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cag	gac	agc	ggc	aag	aga	cga	aag	gtt	gtc	ctg	tcc	agt	cct	agc	caa		384
Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln		
			115				120					125					
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gat		432
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp		
			130			135					140						
ccc	caa	tca	gct	gtt	ctg	gag	aaa	cca	agg	gtt	ctt	gag	caa	cca	ttg		480
Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu		
			145		150				155						160		
gtc	caa	caa	atg	gga	tca	ggt	tca	tcc	ctg	tcg	ggc	aag	caa	aat	tca		528
Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Leu	Ser	Gly	Lys	Gln	Asn	Ser		
				165					170						175		
atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggt	cag	cgg	agg	gtc		576
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val		
			180					185					190				
aat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg		624
Asn	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro		
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gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca		672
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr		
			210			215					220						
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg		720
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser		
				225		230			235						240		
ggc	cta	cct	ctg	aag	tct	tcg	gga	agt	gtg	gac	cct	tcg	cct	gct	aga		768
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg		
				245				250						255			
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga		816
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg		
				260				265					270				
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Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe		
			275				280					285					
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa		912
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu		
			290			295					300						
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc		960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile		
			305		310				315						320		
aag	cag	cag	gat	atc	agg	acc	tct	tcc	tca	aaa	gaa	gag	ccc	tgc	ttc		1008
Lys	Gln	Gln	Asp	Ile	Arg	Thr	Ser	Ser	Ser	Lys	Glu	Glu	Pro	Cys	Phe		

325	330	335	
tct ggt agg aat gca gaa gca gtt	caa gtg cag gat act aag ctc tcc		1056
Ser Gly Arg Asn Ala Glu Ala Val	Gln Val Gln Asp Thr Lys Leu Ser		
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cgg tca gay atg aag aaa atc cgc	aaa gct gag aaa aaa gat aag aag		1104
Arg Ser Asp Met Lys Lys Ile Arg	Lys Ala Glu Lys Lys Asp Lys Lys		
355	360	365	
ttc aga gat ctg ttt gtt acc tgg	aat ccg gta ttg ata gag aat gaa		1152
Phe Arg Asp Leu Phe Val Thr Trp	Asn Pro Val Leu Ile Glu Asn Glu		
370	375	380	
ggg tca gat ctt ggt gat gaa gac	tgg ctg ttc agc agt aaa agg aac		1200
Gly Ser Asp Leu Gly Asp Glu Asp	Trp Leu Phe Ser Ser Lys Arg Asn		
385	390	395	400
tcc gat gct atc atg gtt caa agc	aga gct act gat agt tca gtg ccg		1248
Ser Asp Ala Ile Met Val Gln Ser	Arg Ala Thr Asp Ser Ser Val Pro		
405	410	415	
atc cat cca atg gtg cag cag aag	cct tct tta caa ccc agg gca aca		1296
Ile His Pro Met Val Gln Gln Lys	Pro Ser Leu Gln Pro Arg Ala Thr		
420	425	430	
ttt ttg ccg gac ctt aat atg tac	cag ctg cca tat gtc gta cca ttt		1344
Phe Leu Pro Asp Leu Asn Met Tyr	Gln Leu Pro Tyr Val Val Pro Phe		
435	440	445	
taa			1347
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Met Ser Arg Cys Phe Pro Tyr Pro	Pro Gly Tyr Val Arg Asn Pro		
1	5	10	15
Val Ala Val Ala Glu Pro Glu Ser	Thr Ala Lys Leu Leu Lys Glu Lys		
20	25	30	
Glu Lys Ala Glu Lys Lys Lys Glu	Lys Arg Ser Asp Arg Lys Ala Pro		
35	40	45	
Lys Gln Cys Glu Thr Ser Lys His	Ser Lys His Ser His Lys Lys Arg		
50	55	60	
Lys Leu Glu Asp Val Ile Lys Ala	Glu Gln Gly Pro Lys Arg Val Pro		

65

70

75

80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 49  
<211> 495  
<212> DNA  
<213> Zea mays mays strain Pira

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ccttcggatt tacacacgca cgtgccagat cgttgttcaa tctgtagggt ttgcgcggat 180  
ctgtgggtttg cgcgtgcgtg atgtgggtat tgscctggcc ttgaaagcta accgagctga 240  
ggaagtgtat ggatcttgtg tagctgcacg aggtcctcca aatcgattgt aaaatttaag 300  
ttgtatggsc ggtaggscaa gattgggtta gtccggtttt cgaaaactgg tagcatggtt 360  
atcggggaca ttgaaagaat ggtagaacat caaattcgat tcaaaactgt gctagatttg 420

catatttagt cgccctaaaa ttacgtggac gtgggtgatc cgaattgggtt attgtatgat 480  
 gggttgaata tgagc 495

<210> 50  
 <211> 1768  
 <212> DNA  
 <213> Zea mays mays strain Pira

<400> 50  
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 ctgttgtcag ggaagtaacg tgttcaacat gattgtaaac gaatacattc tgttgctaac 180  
 tgtgtaatga tgagaaggat aattgaataa tctttgtgaa gtattactgt ctgaactgta 240  
 cgcaatgcta cattcattct ttgtgttcgt gtaaataatca ttatacataa aaatgctgct 300  
 tgcattcccg tcgtccgttc taaatcagaa ctgacgattg ctctgggtggc tgaagctcct 360  
 gaaagaaaag gaaaaagccg aaaagaagaa agagaaaagg agtgacagga aagctcccaa 420  
 gcagtgtgag acgtccaaac attcaaagca cagccataag aagagaaagc ttgaagatgt 480  
 catcaaagct gagcagggtc ccaaagagat acccaaagaa tcagttgagc agttggagaa 540  
 gagtggactc tcagaagagc atggagctcc ttcttttgta catacgatac gtgactctcc 600  
 tgagagctca caggacagcg gcaagagacg aaagggtgtc ctgtccagtc ctagccaacc 660  
 taagaatggt gagactattc tcttggtttt gctattctga ttgatttatt attatagaag 720  
 aaatcaatca cttgttcagg attttattca tcccaacttg attttacagg aaacattctt 780  
 cgcttcaaga ttaaaagtag tcaagatccc caatcagctg ttctggagaa accaagggtt 840  
 cttgagcaac cattggtcca acaaagtgga tcaggttcat ccctgtctgg caagcaaaat 900  
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 tcccaagcag tacaaaaatg tttgattaca gaatccccgg caaagaccat gcagagactt 1020  
 gtccccagc ctgcagctaa ggtcacacat cctgttgatc cccagtcagc tgtaaggtg 1080  
 ccagttggaa gatcgggcct acctctgaag tcttcgggaa gtgtggacct ttcgcctgct 1140  
 agagttatga gaagatttga tcctccacct gttaagatga tgtcacagag agttcaccat 1200  
 ccagcttcca tgggtgtcga gaaagttgat cctccgtttc cgaaggtatt acataaggaa 1260  
 accggatctg ttgttcgcct accagaagct acccggccta ctgttcttca aaaaccaag 1320  
 gacttgcctg ctatcaagca gcaggagatc aggacctctt yctcaaaaga agagccctgc 1380

2251220 2405400T

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atgaagaaaa tccgcaaagc tgagaaaaaa gataagaagt tcagagatct gtttgttacc 1500
tggaatccgg tattgataga gaatgaaggt tcagatcttg gtgatgaaga ctggctgttc 1560
agcagtaaaa ggaactccga tgctatcatg gttcaaagca gagctactga tagttcagtg 1620
ccgatccatc caatgggtgca gcagaagcct tctttacaac ccagggcaac atttttgccg 1680
gaccttaata tgtaccagct gccatatgtc gtaccatttt aaacatctgg cgaggtagat 1740
gagaattaga tgagatgttg ggagagag 1768

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<210> 51
<211> 1347
<212> DNA
<213> Zea mays mays strain Pira

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<220>
<221> CDS
<222> (1)..(1347)
<223>

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<400> 51
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1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

gaa aaa gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384

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Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
115 120 125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
130 135 140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	
145 150 155 160	
gtc caa caa atg gga tca ggt tca tcc ctg tct ggc aag caa aat tca	528
Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser	
165 170 175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc	576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	
180 185 190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg	624
Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	
195 200 205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca	672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
210 215 220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg	720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
225 230 235 240	
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga	768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
245 250 255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga	816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	
260 265 270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt	864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	
275 280 285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa	912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	
290 295 300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc	960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
305 310 315 320	
aag cag cag gag atc agg acc tct tyc tca aaa gaa gag ccc tgc ttc	1008
Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe	
325 330 335	
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc	1056
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	



205120" 2406400T

340	345	350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365			1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380			1152
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr 420 425 430			1296
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe 435 440 445			1344
taa			1347

<210> 52  
 <211> 448  
 <212> PRT  
 <213> Zea mays mays strain Pira  
 <220>  
 <221> misc\_feature  
 <222> (329)..(329)  
 <223> The 'Xaa' at location 329 stands for Ser, or Phe.  
 <400> 52

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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys 20 25 30
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro 35 40 45
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60

10070042007

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Xaa Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

&lt;210&gt; 53

&lt;211&gt; 212

&lt;212&gt; DNA

&lt;213&gt; Zea mays mays strain Sari

&lt;400&gt; 53

gcgcggtcga ccgtcggcat gtcgaggtgc ttcccctacc cgccaccggg gtacgtgcgg 60

aaccacagtgg ccgtggccga gccggagtcg accgctaagg tttgttgaac cttcggattt 120

acacacgcac gtgccagatc gtttgttcaa tctgtaggtt ttgcgcggat ctgtggtttg 180

cgcgctgcgtg atgtgggtat tgcccgtgcc tt 212

&lt;210&gt; 54

&lt;211&gt; 1803

&lt;212&gt; DNA

<213> Zea mays mays strain Sari

<400> 54

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tctgtagagt atgcattggt gcaggtctta actgttgtca gggaagtaac gtgttcaaca 180  
tgattgtaaa cgaatacaat tctgttgcta actgtgtaat gatgagaagg ataattgaat 240  
aatctttgtg aagtattact gtctgaactg tacgcaaag ctacattcat tctttgtgtt 300  
cgtgtaaata tcattataca taaaaatgct gcattgcatt cccgtcgtcc gttctaaatc 360  
agaactgacg attgctctgg tggtgaagc tcctgaaaga aaaggaaaag gccgaaaaga 420  
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gagtacccaa agaatcagtt gagcagttgg agaagagtgg actctcagaa gagcatggag 600  
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ttcatcccaa cttgatttta caggaaacat tcttcgcttc aagattaaaa gtagtcaaga 840  
tccccaatca gctgttctgg agaaaccaag ggttcttgag caaccattgg tccaacaaat 900  
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acatcctggt gatccccagt cagctgttaw ggtgccagtt ggaagatcgg gcctacctct 1140  
gaagtcttcg ggaagtgtgg acccttcgcc tgctagagtt atgagaagat ttgatcctcc 1200  
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tatcaggacc tcttcctcaa aagaagagcc ctgcttctct ggtaggaatg cagaagcagt 1440  
tcaagtgcag gatactaagc tctcccggtc agayatgaag aaaatccgca aagctgagaa 1500  
aaaagataag aagttcagag atctgtttgt tacctggaat ccggtattga tagagaatga 1560  
aggttcagat cttggtgatg aagactggct gttcagcagt aaaaggaact ccgatgctat 1620

catggttcaa agcagagcta ctgatagttc agtgccgata catccaatgg tgcagcagaa 1680  
gccttcttta caacccaggg caacattttt gccggacctt aatatgtacc agctgccata 1740  
tgtcgtacca ttttaaacat ctggcgaggt agatgagaat tagatgagat gttgggagag 1800  
agc 1803

<210> 55  
<211> 1347  
<212> DNA  
<213> Zea mays mays strain Sari

<220>  
<221> CDS  
<222> (1)..(1347)  
<223>

<400> 55  
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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
1 5 10 15  
gtg gcc gtg gcc gag ccg gag tgc acc gct aag ctc ctg aaa gaa aag 96  
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
20 25 30  
gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45  
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
50 55 60  
aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80  
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95  
gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110  
cag gac agc gcc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384  
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125  
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432  
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175	528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205	624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220	672
cat cct gtt gat ccc cag tca gct gtt awg gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser 225 230 235 240	720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255	768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270	816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285	864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
tct ggt agg aat gca gaa gca gtt caa gtg car gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350	1056
cgg tca gay atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365	1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
 370 375 380

ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200  
 Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
 385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248  
 Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
 405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296  
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
 420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344  
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
 435 440 445

taa 1347

<210> 56

<211> 448

<212> PRT

<213> Zea mays mays strain Sari

<220>

<221> misc\_feature

<222> (234)..(234)

<223> The 'Xaa' at location 234 stands for Lys, or Met.

<400> 56

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
 20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
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Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
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Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95

206T20" 2405200T

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
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Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
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Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
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His Pro Val Asp Pro Gln Ser Ala Val Xaa Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
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Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320



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Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
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Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

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 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
 20 25 30  
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gat ccc 144  
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Asp Pro  
 35 40 45  
 aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aga 192  
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
 50 55 60  
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80  
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288

Lys	Glu	Ser	Val	Glu	Gln	Leu	Glu	Lys	Ser	Gly	Leu	Ser	Glu	Glu	His	
				85					90					95		
gga	gct	cct	tct	ttt	gta	cat	acg	ata	cgg	gac	tct	cct	gag	agc	tca	336
Gly	Ala	Pro	Ser	Phe	Val	His	Thr	Ile	Arg	Asp	Ser	Pro	Glu	Ser	Ser	
			100					105					110			
cag	gac	agc	ggc	aag	aga	cga	aag	gtt	gtc	ctg	tcc	agt	cct	agc	caa	384
Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln	
			115				120					125				
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gat	432
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp	
	130					135					140					
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Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu	
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Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Leu	Ser	Gly	Lys	Gln	Asn	Ser	
			165						170					175		
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Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val	
			180					185					190			
aat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg	624
Asn	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro	
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gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca	672
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr	
	210					215					220					
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg	720
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser	
225					230				235						240	
ggc	cta	cct	ctg	aag	tct	tca	gga	agt	gtg	gac	cct	tcg	cct	gct	aga	768
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg	
				245					250					255		
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga	816
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg	
			260					265					270			
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Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe	
		275					280					285				
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa	912
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu	
	290					295					300					
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	tct	atc	960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ser	Ile	

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aag cag cag gag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc				1008
Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe				
325		330	335	
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Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser				
340		345	350	
cgg tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag				1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys				
355		360	365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa				1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu				
370		375	380	
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Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn				
385		390	400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg				1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro				
405		410	415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca				1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr				
420		425	430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt				1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe				
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Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Asp Pro				
35 40 45				
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg				

50

55

60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
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Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
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Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

2007-2008

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ser Ile  
305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
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Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
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Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

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- <212> DNA
- <213> Zea mays mays strain W22

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<213> Zea mays mays strain W22

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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
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gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
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aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
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gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336

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Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln	
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Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp	
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Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu	
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Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val	
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Asp	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro	
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Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr	
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His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser	
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Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg	
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Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe	
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Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu	
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gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc	960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile	
		305			310				315						320	
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Lys	Gln	Gln	Asp	Ile	Arg	Thr	Ser	Ser	Ser	Lys	Glu	Glu	Pro	Cys	Phe	

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ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248
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Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg 50 55 60			
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro			

65

70

75

80

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Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser  
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Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
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225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
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Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
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Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
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Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
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Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
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Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45  
aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
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aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
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Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95



gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca	336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser	
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cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa	384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	
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cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat	432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	
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ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg	480
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Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	
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His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	
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Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	
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Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	
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Phe	Leu	Pro	Asp	Leu	Asn	Met	Tyr	Gln	Leu	Pro	Tyr	Val	Val	Pro	Phe		
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Glu	Lys	Ala	Glu	Lys	Lys	Lys	Glu	Lys	Arg	Ser	Asp	Arg	Lys	Ala	Pro		
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Lys	Gln	Cys	Glu	Thr	Ser	Lys	His	Ser	Lys	His	Ser	His	Lys	Lys	Arg		
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Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
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Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
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Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
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Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
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Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
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Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
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Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
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His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
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Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
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Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
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Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
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Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu

290

295

300

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 atttactaat tcttaataca gtatttcggtt attttcgggt aagctt 586

<210> 70  
 <211> 1775  
 <212> DNA  
 <213> Zea mays parviglumis strain BK4

<400> 70  
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 accatttatt gatcccattt ttagttttct tgttctgtag agtatgcatt gttgcaggtc 120  
 ttaactgttg tcaggaagt aacgtgttca acatgattgt aaacgaatac aattctgttg 180  
 ctaactgtgt aatgatgaga aggataattg aataatcttt gtgaagtatt actgtctgaa 240  
 ctgtacgcaa atgctacatt cattctttgt gttcgtgtaa atatcattat acataaaaat 300  
 gctgcattgc attcccgtcg tccgttctaa tcagaactga cgattgctct ggtggctgaa 360  
 gtcctgaaa gaaaaggaaa aggccgaaaa gaagaaagag aaaaggagtg acaggaaagc 420  
 tccaagcag tgtgagacgt ccaaaccattc aaagcacagc cataagaaga gaaagcttga 480  
 agatgtcatc aaagctgagc agggccccaa aagagtacc aaagaatcag ttgagcagtt 540  
 ggagaagagt ggactctcag aagagcatgg agctccttct tttgtacata cgatacgtga 600  
 ctctcctgag agctcacagg acagcggcaa gagacgaaag gttgtcctgt ccagtcctag 660  
 ccaacctaag aatggtgaga ctattctctt gtttttgcta ttctgattga tttttatta 720  
 tagaagaaat caatcgcttg ttcaggattt tattcatccc aacttgattt tacaggaaac 780  
 attcttcgct tcaagattaa aagtagtcaa gacccccaat cagctgttct ggagaaacca 840  
 agggttcttg agcaaccatt ggtccaacaa atgggatcag gttcatcccc gtcgggcaag 900  
 caaaattcaa tccatcataa gatgaatgtg agatctacct ctggtcagcg gaggtcgat 960  
 ggtgactccc aagcagtaca aaaatgtttg attacagaat ccccgcaaa gaccatgcag 1020  
 agacttgctc ccagcctgc agctaaggtc acacatcctg ttgatcccca gtcagctgtt 1080  
 aagggtgccag ttggaagatc gggcctacct ctgaagtctt cgggaagtgt ggacccttcg 1140  
 cctgctagag ttatgagaag atttgatcct ccacctgtta agatgatgtc acagagagtt 1200  
 caccatccag cttocatggt gtcgcagaaa gttgatcctc cgtttccgaa ggtattacat 1260

aaggaaaccg gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa 1320  
 cccaaggact tgcttgctat caagcagcag gatatcagga cctcttctctc aaaagaagag 1380  
 ccctgcttct ctggtaggaa tgcagaagca gttcaagtgc aagatactaa gctctcccgg 1440  
 tcagacatga agaaaatccg caaagctgag aaaaaagata agaagttcag agatctgttt 1500  
 gttacctgga atccggtatt gatagagaat gaaggttcag atcttggtga tgaagactgg 1560  
 ctgttcagca gtaaaaggaa ctccgatgct atcatggttc aaagcagagc tactgatagt 1620  
 tcagtgccga tccatccaat ggtgcagcag aagccttctt tacaaccag ggcaacattt 1680  
 ttgccggacc ttaatatgta ccagctgcc aatgtcgtag cattttaaac atctggcgag 1740  
 gtagatgaga attagatgag atgttgggag agagc 1775

<210> 71  
 <211> 1347  
 <212> DNA  
 <213> Zea mays parviglumis strain BK4

<220>  
 <221> CDS  
 <222> (1)..(1347)  
 <223>

<400> 71  
 atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48  
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
 1 5 10 15  
 gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96  
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
 20 25 30  
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
 35 40 45  
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
 50 55 60  
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80  
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95  
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser

	100	105	110	
cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa				384
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln	115	120	125	
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gac				432
Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp	130	135	140	
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg				480
Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu	145	150	155	160
gtc caa caa atg gga tca ggt tca tcc ccg tcg ggc aag caa aat tca				528
Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser	165	170	175	
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc				576
Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val	180	185	190	
gat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg				624
Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro	195	200	205	
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca				672
Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr	210	215	220	
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg				720
His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser	225	230	235	240
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga				768
Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg	245	250	255	
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga				816
Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg	260	265	270	
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt				864
Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe	275	280	285	
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa				912
Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu	290	295	300	
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc				960
Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile	305	310	315	320
aag cag cag gat atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc				1008
Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe	325	330	335	

tct ggt agg aat gca gaa gca gtt caa gtg caa gat act aag ctc tcc 1056  
Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104  
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152  
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200  
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248  
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296  
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344  
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

taa 1347

<210> 72  
<211> 448  
<212> PRT  
<213> Zea mays parviglumis strain BK4

<400> 72

Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
1 5 10 15

Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys  
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80



Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Pro Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asp Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

206T20 2406200T

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 73

<211> 305

<212> DNA

<213> Zea mays parviglumis strain IA19

<400> 73

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cgtcggccat gtcgaggtgc ttccctacc cgccaccggg gtacgtgcgg aaccagtggt 120

ccgtggccga gccggagtcg accgctaagg tttgttgaac cttcggattt acacacgcac 180

gtgccagatc gtttgttcaa tctgtagggt ttgcgcggat ctgtggtttg cgcgtgcgtg 240

atgtgggtat tgcccgtgcc ttgaaagcta accgagctga ggaagtgtat ggatcttgtg 300

tagct 305

<210> 74

<211> 1309  
 <212> DNA  
 <213> Zea mays parviglumis strain IA19

<400> 74

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aaaagagtac ccaaagaatc agttgagcag ttggagaaga gtggactctc agaagagcat	120
ggagctcctt cttttgtaca tacgatacgt gactctcctg agagctcaca ggacagcggc	180
aagagacgaa aggttgtcct gtccagtcct agccaacctt agaatggtga gactattctc	240
ttgtttttgc tattctgatt gattttttat tatagaagaa atcaatcgct tgttcaggat	300
tttattcatc ccaacttgat ttacaggaa acattcttctg cttcaagatt aaaagtagtc	360
aagatcccca atcagctgtt ctggagaaac caagggttct tgagcaacca ttggtccaac	420
aatggggtc aggttcatcc ctgtcgggca agcaaaattc aatccatcat aagatgaatg	480
tgagatctac ctctggtcag cggaggggtca atgggtgactc ccaagcagta caaaaatgtt	540
tgattacaga atccccggca aagaccatgc agagacttgt cccccagcct gcagctaagg	600
tcacacatcc tgttgatccc cagtcagctg ttaaggtgcc agttggaaga tcgggcctac	660
ctctgaagtc ttcgggaagt gtggaccctt cgctgctag agttatgaga agatttgatc	720
ctccacctgt taagatgatg tcacagagag ttcaccatcc agcttccatg gtgtcgcaga	780
aagttgatcc tccgtttccg aaggtattac ataaggaaac cggatctgtt gttcgcctac	840
cagaagctac ccggcctact gttcttcaaa aacccaagga cttgcctgct atcaagcagc	900
aggakatcag gacctcttcc tcaaaagaag agccctgctt ctctggtagg aatgcagaag	960
cagttcaagt gcaggatact aagctctccc ggtcagacat gaagaaaatc cgcaaagctg	1020
agaaaaaaga taagaagttc agagatctgt ttgttacctg gaatccggtg ttgatagaga	1080
atgaagggtc agatcttggt gatgaagact ggctgttcag cagtaaaagg aactccgatg	1140
ctatcatggt tcaaagcaga gctactgata gttcagtgcc gatccatcca atgggtgcagc	1200
agaagccttc tttaacaacc agggcaacat ttttgccgga ccttaatatg taccagctgc	1260
catatgtcgt accattttta acatctgtcg aggtagatga gaattagat	1309

<210> 75  
 <211> 1347  
 <212> DNA  
 <213> Zea mays parviglumis strain IA19

<220>  
 <221> CDS

<222> (1)..(1332)  
 <223>

<220>  
 <221> misc\_feature  
 <222> (82)..(168)  
 <223> n = A, C, T, or G

<400> 75  
 atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48  
 Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro  
 1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag nnn nnn nnn nnn nnn 96  
 Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa  
 20 25 30

nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn 144  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40 45

nnn nnn nnn nnn nnn nnn nnn nnn tca aag cac agc cat aag aag aga 192  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg  
 50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag gtt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro  
 65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
 100 105 110

cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384  
 Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
 115 120 125

cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat 432  
 Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
 130 135 140

ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg 480  
 Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
 145 150 155 160

gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca 528  
 Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
 165 170 175

atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc 576  
 Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val

180	185	190	
aat ggt gac tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205			624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220			672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240			720
ggc cta cct ctg aag tct tcg gga agt gtg gac cct tcg cct gct aga Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg 245 250 255			768
gtt atg aga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270			816
gtt cac cat cca gct tcc atg gtg tcg cag aaa gtt gat cct ccg ttt Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe 275 280 285			864
ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300			912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320			960
aag cag cag gak atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Xaa Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335			1008
tct ggt agg aat gca gaa gca gtt caa gtg cag gat act aag ctc tcc Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser 340 345 350			1056
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys 355 360 365			1104
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu 370 375 380			1152
ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn 385 390 395 400			1200
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro 405 410 415			1248

atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca 1296  
 Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
           420                          425                          430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtcgtacccat tttaa 1347  
 Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr  
           435                          440

<210> 76  
 <211> 444  
 <212> PRT  
 <213> Zea mays parviglumis strain IA19

<220>  
 <221> misc\_feature  
 <222> (28)..(28)  
 <223> The 'Xaa' at location 28 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (29)..(29)  
 <223> The 'Xaa' at location 29 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (30)..(30)  
 <223> The 'Xaa' at location 30 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (31)..(31)  
 <223> The 'Xaa' at location 31 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (32)..(32)  
 <223> The 'Xaa' at location 32 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (33)..(33)  
 <223> The 'Xaa' at location 33 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
           Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
           Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (34)..(34)  
<223> The 'Xaa' at location 34 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (35)..(35)  
<223> The 'Xaa' at location 35 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (36)..(36)  
<223> The 'Xaa' at location 36 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (37)..(37)  
<223> The 'Xaa' at location 37 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (38)..(38)  
<223> The 'Xaa' at location 38 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (39)..(39)  
<223> The 'Xaa' at location 39 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (40)..(40)  
<223> The 'Xaa' at location 40 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (41)..(41)  
<223> The 'Xaa' at location 41 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>

205120" 24052001

<221> misc\_feature  
<222> (42)..(42)  
<223> The 'Xaa' at location 42 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (43)..(43)  
<223> The 'Xaa' at location 43 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (44)..(44)  
<223> The 'Xaa' at location 44 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (45)..(45)  
<223> The 'Xaa' at location 45 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (46)..(46)  
<223> The 'Xaa' at location 46 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (47)..(47)  
<223> The 'Xaa' at location 47 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (48)..(48)  
<223> The 'Xaa' at location 48 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature  
<222> (49)..(49)  
<223> The 'Xaa' at location 49 stands for Lys, Asn, Arg, Ser, Thr, Ile,  
Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,  
Tyr, Trp, Cys, or Phe.

<220>  
<221> misc\_feature



<222> (50)..(50)  
 <223> The 'Xaa' at location 50 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (51)..(51)  
 <223> The 'Xaa' at location 51 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (52)..(52)  
 <223> The 'Xaa' at location 52 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (53)..(53)  
 <223> The 'Xaa' at location 53 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (54)..(54)  
 <223> The 'Xaa' at location 54 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (55)..(55)  
 <223> The 'Xaa' at location 55 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (56)..(56)  
 <223> The 'Xaa' at location 56 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>  
 <221> misc\_feature  
 <222> (324)..(324)  
 <223> The 'Xaa' at location 324 stands for Glu, or Asp.

<220>  
 <221> misc\_feature  
 <222> (82)..(168)  
 <223> n = A, C, T, or G

<400> 76

Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro  
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Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Xaa Xaa Xaa Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Lys His Ser His Lys Lys Arg  
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Val Pro Lys Arg Val Pro  
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

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His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Xaa Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr  
435 440

<210> 77  
 <211> 86  
 <212> DNA  
 <213> Zea mays parviglumis strain Wilkes

<400> 77  
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 caccggggta cgtgcggaac ccagtg 86

<210> 78  
 <211> 1347  
 <212> DNA  
 <213> Zea mays parviglumis strain Wilkes

<220>  
 <221> misc\_feature  
 <222> (52)..(81)  
 <223> N = A, C, G, or T

<220>  
 <221> CDS  
 <222> (1)..(1347)  
 <223>

<400> 78  
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 Met Ser Arg Cys Phe Pro Tyr Pro Pro Gly Tyr Val Arg Asn Pro  
 1 5 10 15  
 gtg nnn nnn nnn nnn nnn nnn nnn nnn nnn nnn ctc ctg aaa gaa aag 96  
 Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys  
 20 25 30  
 gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144  
 Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
 35 40 45  
 aag cag tgt gag acg tcc aaa cat tca aag cac agc cat aag aag aga 192  
 Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
 50 55 60  
 aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240  
 Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80  
 aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
 Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95  
 gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336  
 Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
 100 105 110

cag	gac	agc	ggc	aag	aga	cga	aag	gtt	gtc	ctg	tcc	agt	cct	agc	caa	384
Gln	Asp	Ser	Gly	Lys	Arg	Arg	Lys	Val	Val	Leu	Ser	Ser	Pro	Ser	Gln	
		115					120					125				
cct	aag	aat	gga	aac	att	ctt	cgc	ttc	aag	att	aaa	agt	agt	caa	gat	432
Pro	Lys	Asn	Gly	Asn	Ile	Leu	Arg	Phe	Lys	Ile	Lys	Ser	Ser	Gln	Asp	
		130				135					140					
ccc	caa	tca	gct	gtt	ctg	gag	aaa	cca	agg	gtt	ctt	gag	caa	cca	ttg	480
Pro	Gln	Ser	Ala	Val	Leu	Glu	Lys	Pro	Arg	Val	Leu	Glu	Gln	Pro	Leu	
145					150					155					160	
gtc	caa	caa	atg	gga	tca	ggt	tca	tcc	ctg	tcg	ggc	aag	caa	aat	tca	528
Val	Gln	Gln	Met	Gly	Ser	Gly	Ser	Ser	Leu	Ser	Gly	Lys	Gln	Asn	Ser	
				165					170					175		
atc	cat	cat	aag	atg	aat	gtg	aga	tct	acc	tct	ggg	cag	cgg	agg	gtc	576
Ile	His	His	Lys	Met	Asn	Val	Arg	Ser	Thr	Ser	Gly	Gln	Arg	Arg	Val	
			180					185					190			
aat	ggt	gac	tcc	caa	gca	gta	caa	aaa	tgt	ttg	att	aca	gaa	tcc	ccg	624
Asn	Gly	Asp	Ser	Gln	Ala	Val	Gln	Lys	Cys	Leu	Ile	Thr	Glu	Ser	Pro	
		195					200					205				
gca	aag	acc	atg	cag	aga	ctt	gtc	ccc	cag	cct	gca	gct	aag	gtc	aca	672
Ala	Lys	Thr	Met	Gln	Arg	Leu	Val	Pro	Gln	Pro	Ala	Ala	Lys	Val	Thr	
		210				215					220					
cat	cct	gtt	gat	ccc	cag	tca	gct	gtt	aag	gtg	cca	gtt	gga	aga	tcg	720
His	Pro	Val	Asp	Pro	Gln	Ser	Ala	Val	Lys	Val	Pro	Val	Gly	Arg	Ser	
225					230					235					240	
ggc	cta	cct	ctg	aag	tct	tcg	gga	agt	gtg	gac	cct	tcg	cct	gct	aga	768
Gly	Leu	Pro	Leu	Lys	Ser	Ser	Gly	Ser	Val	Asp	Pro	Ser	Pro	Ala	Arg	
				245					250					255		
gtt	atg	aga	aga	ttt	gat	cct	cca	cct	gtt	aag	atg	atg	tca	cag	aga	816
Val	Met	Arg	Arg	Phe	Asp	Pro	Pro	Pro	Val	Lys	Met	Met	Ser	Gln	Arg	
			260					265					270			
gtt	cac	cat	cca	gct	tcc	atg	gtg	tcg	cag	aaa	gtt	gat	cct	ccg	ttt	864
Val	His	His	Pro	Ala	Ser	Met	Val	Ser	Gln	Lys	Val	Asp	Pro	Pro	Phe	
		275					280					285				
ccg	aag	gta	tta	cat	aag	gaa	acc	gga	tct	gtt	gtt	cgc	cta	cca	gaa	912
Pro	Lys	Val	Leu	His	Lys	Glu	Thr	Gly	Ser	Val	Val	Arg	Leu	Pro	Glu	
		290				295					300					
gct	acc	cgg	cct	act	gtt	ctt	caa	aaa	ccc	aag	gac	ttg	cct	gct	atc	960
Ala	Thr	Arg	Pro	Thr	Val	Leu	Gln	Lys	Pro	Lys	Asp	Leu	Pro	Ala	Ile	
305					310				315						320	
aag	cag	cag	gat	atc	agg	acc	tct	tcc	tca	aaa	gaa	gag	ccc	tgc	ttc	1008

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser	
340 345 350	
cgg tca gac atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag	1104
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys	
355 360 365	
ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa	1152
Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu	
370 375 380	
ggg tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac	1200
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn	
385 390 395 400	
tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg	1248
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro	
405 410 415	
atc cat cca atg gtg cag cag aag cct tct tta caa ccc agg gca aca	1296
Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr	
420 425 430	
ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt	1344
Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe	
435 440 445	
taa	1347

<210> 79  
 <211> 448  
 <212> PRT  
 <213> Zea mays parviglumis strain Wilkes  
  
 <220>  
 <221> misc\_feature  
 <222> (18)..(18)  
 <223> The 'Xaa' at location 18 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.  
  
 <220>  
 <221> misc\_feature  
 <222> (19)..(19)  
 <223> The 'Xaa' at location 19 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.  
  
 <220>  
 <221> misc\_feature  
 <222> (20)..(20)  
 <223> The 'Xaa' at location 20 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.  
  
 <220>

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<221> misc_feature
<222> (21)..(21)
<223> The 'Xaa' at location 21 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (22)..(22)
<223> The 'Xaa' at location 22 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (23)..(23)
<223> The 'Xaa' at location 23 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (24)..(24)
<223> The 'Xaa' at location 24 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (25)..(25)
<223> The 'Xaa' at location 25 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (26)..(26)
<223> The 'Xaa' at location 26 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (27)..(27)
<223> The 'Xaa' at location 27 stands for Lys, Asn, Arg, Ser, Thr, Ile,
      Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon,
      Tyr, Trp, Cys, or Phe.

<220>
<221> misc_feature
<222> (52)..(81)
<223> N = A, C, G, or T

<400> 79

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Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1          5                      10                      15

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Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Leu Lys Glu Lys  
20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240



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Gly Leu Pro Leu Lys Ser Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Arg Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Phe  
275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Asp Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

Phe Leu Pro Asp Leu Asn Met Tyr Gln Leu Pro Tyr Val Val Pro Phe  
435 440 445

<210> 80  
<211> 225  
<212> DNA  
<213> Zea diploperennis

<400> 80  
 agcgcggtcg accgtcggcc atgtcgaggt gcttccccta cccgccaccg gggtagctgc 60  
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 ttacacacgc acgtgccaga tcgtttgttc aatctgtagg ttttgccgcg atctgtgggt 180  
 tgcgcgtgcg tgatgtgggt attgcccgtg ccttgaaagc taacc 225

<210> 81  
 <211> 1672  
 <212> DNA  
 <213> Zea diploperennis

<400> 81  
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 atgatgagaa ggataattga ataatctttg tgaagtatta ctgtctgaac tgtacgcaaa 180  
 tgctacattc attctttgtg ttcgtgtaaa tatcattata cataaaaaatg ctgcattgca 240  
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 gaaaaggaaa aggccgaaaa gaagaaagag aaaaggagtg acaggaaagc tcccaagcag 360  
 tgtgagacgt ccaaacactc aaagcacagc cataagaaga gaaagcttga agatgtcatc 420  
 aaagctgagc aggggtccaa aagagtacc aaagaatcag ttgagcagtt ggagaagagt 480  
 ggactctcag aagagcatgg agctccttct tttgtacata cgatacgtga ctctcctgag 540  
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 aatggtgaga ctattctctt gtttttgcta ttctgattga ttttttatta tagaagaaat 660  
 caatcacttg ttcaggattt tattcatccc aacttgattt tacaggaaac attcttcgct 720  
 tcaagattaa aagtagtcaa gatccccaat cagctgttct ggagaaacca agggttcttg 780  
 agcaaccatt ggtccaacaa atgggatcag gttcatccct gtcgggcaag caaaattcaa 840  
 tccatcataa gatgaatgtg agatctacct ctggtcagcg gagggccaat ggtgactcgc 900  
 aagcagtaca aaaatgtttg attacagaat ccccggaacaa gaccatgcag agacttgtcc 960  
 cccagcctgc agctaaggct acacatcctg ttgatcccca gtcagctgtt aaggtgccag 1020  
 ttggaaggct gggcctacct ctcaagtttt cggaagatg ggacccttcg cctgctagag 1080  
 ttatgggaag atttgatcct ccacctgtta agatgatgtc acagagagtt caccatccag 1140  
 cttccatggt gtcgcagaaa gttgatcctc cgttaccgaa ggtattacat aaggaaaccg 1200

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gatctgttgt tcgcctacca gaagctaccc ggcctactgt tcttcaaaaa cccaaggact 1260
tgcctgctat caagcagcag cagatcagga cctcttcctc aaaagaagag ccctgcttct 1320
ctggtaggaa tgcagaagca gttcaagtgc atgatactaa gctctcccgg tcagatatga 1380
agaaaatccg caaagctgag aaaaaagata agaagttcag agatctgttt gttacctgga 1440
atccggtatt gatagagaat gaaggttcag atcttggtga tgaagactgg ctgttcagca 1500
gtaaaaggaa ctccgatgct atcatgggtc aaagcagagc tactgatagt tcagtgccga 1560
tccatccaat kgtgcagcag aaaccttctt tacaaccag ggcaacattt ttgccggacc 1620
ttaatatgta ccagctgccca tatgtcgtac cattttaaac atctgtcgag gt 1672

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<210> 82
<211> 1347
<212> DNA
<213> Zea diploperennis

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<220>
<221> CDS
<222> (1)..(1347)
<223>

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<400> 82
atg tcg agg tgc ttc ccc tac ccg cca ccg ggg tac gtg cgg aac cca 48
Met Ser Arg Cys Phe Pro Tyr Pro Pro Pro Gly Tyr Val Arg Asn Pro
1 5 10 15

gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ctg aaa gaa aag 96
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Leu Lys Glu Lys
20 25 30

gaa aag gcc gaa aag aag aaa gag aaa agg agt gac agg aaa gct ccc 144
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro
35 40 45

aag cag tgt gag acg tcc aaa cac tca aag cac agc cat aag aag aga 192
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg
50 55 60

aag ctt gaa gat gtc atc aaa gct gag cag ggt ccc aaa aga gta ccc 240
Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro
65 70 75 80

aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His
85 90 95

gga gct cct tct ttt gta cat acg ata cgt gac tct cct gag agc tca 336
Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser
100 105 110

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cag gac agc ggc aag aga cga aag gtt gtc ctg tcc agt cct agc caa Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln 115 120 125	384
cct aag aat gga aac att ctt cgc ttc aag att aaa agt agt caa gat Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp 130 135 140	432
ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gag caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu 145 150 155 160	480
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atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190	576
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ccg aag gta tta cat aag gaa acc gga tct gtt gtt cgc cta cca gaa Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu 290 295 300	912
gct acc cgg cct act gtt ctt caa aaa ccc aag gac ttg cct gct atc Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile 305 310 315 320	960
aag cag cag cag atc agg acc tct tcc tca aaa gaa gag ccc tgc ttc Lys Gln Gln Gln Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe 325 330 335	1008
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Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser  
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cgg tca gat atg aag aaa atc cgc aaa gct gag aaa aaa gat aag aag 1104  
Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

ttc aga gat ctg ttt gtt acc tgg aat ccg gta ttg ata gag aat gaa 1152  
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370 375 380

ggt tca gat ctt ggt gat gaa gac tgg ctg ttc agc agt aaa agg aac 1200  
Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

tcc gat gct atc atg gtt caa agc aga gct act gat agt tca gtg ccg 1248  
Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

atc cat cca atk gtg cag cag aaa cct tct tta caa ccc agg gca aca 1296  
Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

ttt ttg ccg gac ctt aat atg tac cag ctg cca tat gtc gta cca ttt 1344  
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435 440 445

taa 1347

<210> 83  
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<212> PRT  
<213> Zea diploperennis

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<222> (420)..(420)  
<223> The 'Xaa' at location 420 stands for Met, or Ile.

<400> 83

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20 25 30

Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ser His Lys Lys Arg  
50 55 60

Lys Leu Glu Asp Val Ile Lys Ala Glu Gln Gly Pro Lys Arg Val Pro  
65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95

Gly Ala Pro Ser Phe Val His Thr Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Ser Gln Asp  
130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Glu Gln Pro Leu  
145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
180 185 190

Asn Gly Asp Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Met Asp Pro Ser Pro Ala Arg  
245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu  
275 280 285

206T20"2405200T

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
305 310 315 320

Lys Gln Gln Gln Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val His Asp Thr Lys Leu Ser  
340 345 350

Arg Ser Asp Met Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
370 375 380

Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
385 390 395 400

Ser Asp Ala Ile Met Val Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
405 410 415

Ile His Pro Xaa Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
420 425 430

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435 440 445

<210> 84  
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<212> DNA  
<213> Zea luxurians

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cagatcgttt ggtcaatctg ttggttttgc gcggatctgt ggtttgcgcg tgcgtgatgt 180  
gggtattgcc cgtgccttga aagctaaccg agatgaggaa gtgtatggat cttgttttagc 240  
tgcacgaggt cctccaaatc gattgaaaaa tttaagttgg atggccggtg ggccaagatt 300  
gggttagtcc ggtttttgat aactgggtacc atggttatcg gggacattga acagaacggt 360

agaacatcaa attcgattca aaactgtgct agatttgac atttagtcgc cctaagatta	420
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tttgatcctc cacctgttaa gatgatgtca cagagagttc accatccagc ttccatggtg	1860
tcgcagaaaag ttgatccctc gttaccgaag gtattacata aggaaaccgg atctgttggt	1920
cgctaccag aagctaccgg gcctactgtt cttcaaaaac ccaaggactt gcctgctatc	1980
aagcagcagg agatcaggac ctcttctctc aaagaagagc cctgcttctc tggtaggaat	2040



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gtg gcc gtg gcc gag ccg gag tcg acc gct aag ctc ccg aaa gaa aag 96  
Val Ala Val Ala Glu Pro Glu Ser Thr Ala Lys Leu Pro Lys Glu Lys  
20 25 30  
gaa aag gcc gaa aag aag aaa gag aaa ccg agt gac agg aaa gct ccc 144  
Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
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aag cag tgt gag acg tcc aaa cat tca aag cac atc cat aag aag aga 192  
Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg  
50 55 60  
aag ctt gaa gat gtc atc aaa gct ggg cag ggt ccc aaa aga gta ccc 240  
Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro  
65 70 75 80  
aaa gaa tca gtt gag cag ttg gag aag agt gga ctc tca gaa gag cat 288  
Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
85 90 95  
gga gct cct tct ttt gta cat aag ata cgc gac tct cct gag agc tca 336  
Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser  
100 105 110  
cag gac agc gcc aag aga cga aag gtt gtc ctg tcc agt cct agc caa 384  
Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln

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ccc caa tca gct gtt ctg gag aaa cca agg gtt ctt gac caa cca ttg Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu 145 150 155 160			480
gtc caa caa atg gga tca ggt tca tcc ctg tcg ggc aag caa aat tca Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser 165 170 175			528
atc cat cat aag atg aat gtg aga tct acc tct ggt cag cgg agg gtc Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val 180 185 190			576
aat ggt gaa tcc caa gca gta caa aaa tgt ttg att aca gaa tcc ccg Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro 195 200 205			624
gca aag acc atg cag aga ctt gtc ccc cag cct gca gct aag gtc aca Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr 210 215 220			672
cat cct gtt gat ccc cag tca gct gtt aag gtg cca gtt gga aga tcg His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser 225 230 235 240			720
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gtt atg gga aga ttt gat cct cca cct gtt aag atg atg tca cag aga Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg 260 265 270			816
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205120" 24052001

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 385 390 395 400

tcc gat gct atc atg gct caa agc aga gct act gat agt tca gtg ccg 1248  
 Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
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taa 1347

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- <211> 448
- <212> PRT
- <213> Zea luxurians
- <400> 86

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Glu Lys Ala Glu Lys Lys Lys Glu Lys Arg Ser Asp Arg Lys Ala Pro  
 35 40 45

Lys Gln Cys Glu Thr Ser Lys His Ser Lys His Ile His Lys Lys Arg  
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Lys Leu Glu Asp Val Ile Lys Ala Gly Gln Gly Pro Lys Arg Val Pro  
 65 70 75 80

Lys Glu Ser Val Glu Gln Leu Glu Lys Ser Gly Leu Ser Glu Glu His  
 85 90 95

Gly Ala Pro Ser Phe Val His Lys Ile Arg Asp Ser Pro Glu Ser Ser  
 100 105 110

Gln Asp Ser Gly Lys Arg Arg Lys Val Val Leu Ser Ser Pro Ser Gln  
 115 120 125

Pro Lys Asn Gly Asn Ile Leu Arg Phe Lys Ile Lys Ser Asn Gln Asp  
 130 135 140

Pro Gln Ser Ala Val Leu Glu Lys Pro Arg Val Leu Asp Gln Pro Leu  
 145 150 155 160

Val Gln Gln Met Gly Ser Gly Ser Ser Leu Ser Gly Lys Gln Asn Ser  
 165 170 175

Ile His His Lys Met Asn Val Arg Ser Thr Ser Gly Gln Arg Arg Val  
 180 185 190

Asn Gly Glu Ser Gln Ala Val Gln Lys Cys Leu Ile Thr Glu Ser Pro  
 195 200 205

Ala Lys Thr Met Gln Arg Leu Val Pro Gln Pro Ala Ala Lys Val Thr  
 210 215 220

His Pro Val Asp Pro Gln Ser Ala Val Lys Val Pro Val Gly Arg Ser  
 225 230 235 240

Gly Leu Pro Leu Lys Phe Ser Gly Ser Val Asp Pro Ser Pro Ala Arg  
 245 250 255

Val Met Gly Arg Phe Asp Pro Pro Pro Val Lys Met Met Ser Gln Arg  
 260 265 270

Val His His Pro Ala Ser Met Val Ser Gln Lys Val Asp Pro Pro Leu  
 275 280 285

Pro Lys Val Leu His Lys Glu Thr Gly Ser Val Val Arg Leu Pro Glu  
 290 295 300

Ala Thr Arg Pro Thr Val Leu Gln Lys Pro Lys Asp Leu Pro Ala Ile  
 305 310 315 320

Lys Gln Gln Glu Ile Arg Thr Ser Ser Ser Lys Glu Glu Pro Cys Phe  
 325 330 335

Ser Gly Arg Asn Ala Glu Ala Val Gln Val Gln Asp Thr Lys Leu Ser  
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Arg Ser Asp Val Lys Lys Ile Arg Lys Ala Glu Lys Lys Asp Lys Lys  
 355 360 365

Phe Arg Asp Leu Phe Val Thr Trp Asn Pro Val Leu Ile Glu Asn Glu  
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Gly Ser Asp Leu Gly Asp Glu Asp Trp Leu Phe Ser Ser Lys Arg Asn  
 385 390 395 400

Ser Asp Ala Ile Met Ala Gln Ser Arg Ala Thr Asp Ser Ser Val Pro  
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Ile His Pro Met Val Gln Gln Lys Pro Ser Leu Gln Pro Arg Ala Thr  
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